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Marvich, Maria
Thursday, November 11, 2004 6:27 AM
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10/820133

Please search SEQ ID NO 39-43 and 1-5

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Maria Bonovich Marvich

United States Patent and Trademark Office

Remsen 2B84

AU 1636

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571-272-0774

39-NA - 25
40- / - 25
41- / - 25
42- / - 25
43-NA - 25
1-NA - 25
2- / - 25
3- / - 25
4- / - 25
5-NA - 25

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Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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11/19

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Type of Search

NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
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Matches 21; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AGCCWGCCTTYYKTRTACNAACTSG 25

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ACCESSION ARI24523
VERSION ARI24523.1 GI:14109884
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REFERENCE
1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6171861-A 3 09-JAN-2001;
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DEFINITION Sequence 4 from patent US 6171861.
ACCESSION ARI24524
VERSION ARI24524.1 GI:14109885
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6171861-A 4 09-JAN-2001;
FEATURES Location/Qualifiers
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JOURNAL Patent: US 6171861-A 2 09-JAN-2001;
FEATURES Location/Qualifiers
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JOURNAL Patent: US 6171861-A 5 09-JAN-2001;
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DEFINITION Sequence 1 from patent US 6270969.
ACCESSION ARI63172
VERSION ARI63172.1 GI:16233677
KEYWORDS
SOURCE
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REFERENCE
1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6270969-A 1 07-AUG-2001;
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ACCESSION ARI63173
VERSION ARI63173.1 GI:16233679
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6270969-A 2 07-AUG-2001;
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DEFINITION Sequence 3 from patent US 6270969.
ACCESSION AR163174
VERSION AR163174.1 GI:16233681
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6270969-A 3 07-AUG-2001;
FEATURES Location/Qualifiers
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RESULT 9
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DEFINITION Sequence 4 from patent US 6270969.
ACCESSION AR163175
VERSION AR163175.1 GI:16233683
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6270969-A 4 07-AUG-2001;
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DEFINITION Sequence 5 from patent US 6270969.
ACCESSION AR163176
VERSION AR163176.1 GI:16233684
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6270969-A 5 07-AUG-2001;
FEATURES Location/Qualifiers
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Best Local Similarity 80.0%; Pred. No. 46;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 1 from patent US 6720140.
ACCESSION AR493773
VERSION AR493773.1 GI:47266182
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6720140-A 1 13-APR-2004;
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DEFINITION Sequence 2 from patent US 6720140.
ACCESSION AR493774
VERSION AR493774.1 GI:47266184
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6720140-A 2 13-APR-2004;
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DEFINITION Sequence 3 from patent US 6720140.
ACCESSION AR493775
VERSION AR493775.1 GI:47266186
KEYWORDS
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REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6720140-A 3 13-APR-2004;
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DEFINITION Sequence 4 from patent US 6720140.
ACCESSION AR493776
VERSION AR493776.1 GI:47266188
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6720140-A 4 13-APR-2004;
FEATURES
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RESULT 15
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LOCUS
DEFINITION Sequence 5 from patent US 6720140.
ACCESSION AR493777
VERSION AR493777.1 GI:47266190
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6720140-A 5 13-APR-2004;
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OM nucleic - nucleic search, using sw model

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Title: US-10-820-133-1

Perfect score: 25

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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9	19.6	78.4	25	2 AAX78936	Aax78936 Oligonucl
10	19.6	78.4	25	2 AAX78976	Aax78976 Oligonucl
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28	19.6	78.4	25	4 AAD14430	Aad14430 Recombina
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31	19.6	78.4	25	5 AAS14783	Aas14783 Lambda ph
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33	19.6	78.4	25	8 ABT16623	Abt16623 Artificia
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ALIGNMENTS

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XX AAT48212;

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XX 20-OCT-1997 (first entry)

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XX DE M-attr core region.

XX XX

XX att recombination site; core region; mutation; enhance; recombination;

XX vector; subcloning; regulation; exchange; ss.

XX OS Synthetic.

XX XX

XX WO9640724-A1.

XX XX

XX PD 19-DEC-1996.

XX XX

XX PF 07-JUN-1996; 96WO-US010082.

XX XX

XX PR 07-JUN-1995; 95US-00486139.

XX XX

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX PA

XX XX

XX PI Hartley JL, Brasch MA;

XX XX

XX DR WPI; 1997-065168/06.

XX XX

XX PT Nucleic acids, vectors and methods to obtain chimeric nucleic acid -

XX PT using recombinant proteins and engineered recombination sites in vitro or

XX PT in vivo.

XX XX

XX FS Claim 14; Page 55; 106pp; English.

XX XX

XX CC AAT48210-25 are att recombination site core region DNA sequences. The

XX CC core region has at least one engineered mutation that enhances

XX CC recombination in vitro in the formation of a Cointegrate or Product DNA.

XX CC These core regions can be incorporated into novel vector donor DNA

XX CC molecules. The nucleic acids, vectors and methods of the invention are

XX CC used to obtain chimeric nucleic acid using recombination proteins and

XX CC engineered recombination sites in vitro or in vivo. The improved

XX CC specificity, speed and yields of the invention facilitates DNA or RNA

XX CC subcloning, regulation or exchange useful for any related purpose, e.g.

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CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
CC or modification of transcribed, replicated, isolated or genomic DNA or
CC RNA
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SQ Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 5 Other;

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AC AAT48210;
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DT 20-OCT-1997 (first entry)
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DE M-att core region.
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att recombination site; core region; mutation; enhance; recombination;
KW vector; subcloning; regulation; exchange; ss.
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OS Synthetic.
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PN WO9640724-A1.
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PD 19-DEC-1996.
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PF 07-JUN-1996; 96WO-US010082.
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PR 07-JUN-1995; 95US-00486139.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Hartley JL, Brasch MA;
XX
WPI; 1997-065168/06.
XX
Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
PT using recombinant proteins and engineered recombination sites in vitro or
PT in vivo.
XX
PS Claim 14; Page 55; 106pp; English.
XX
AAT48210-25 are att recombination site core region DNA sequences. The
CC core region has at least one engineered mutation that enhances
CC recombination in vitro in the formation of a Cointegrate or Product DNA.
CC These core regions can be incorporated into novel vector donor DNA
CC molecules. The nucleic acids, vectors and methods of the invention are
CC used to obtain chimeric nucleic acid using recombination proteins and
CC engineered recombination sites in vitro or in vivo. The improved
CC specificity, speed and yields of the invention facilitates DNA or RNA
CC subcloning, regulation or exchange useful for any related purpose, e.g.
CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
CC or modification of transcribed, replicated, isolated or genomic DNA or
CC RNA
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SQ Sequence 25 BP; 3 A; 3 C; 2 G; 6 T; 0 U; 11 Other;

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DT 20-OCT-1997 (first entry)
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KW vector; subcloning; regulation; exchange; ss.
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OS Synthetic.
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PD 19-DEC-1996.
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PF 07-JUN-1996; 96WO-US010082.
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PR 07-JUN-1995; 95US-00486139.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
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PI Hartley JL, Brasch MA;
XX
WPI; 1997-065168/06.
XX
Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
PT using recombinant proteins and engineered recombination sites in vitro or
PT in vivo.
XX
PS Claim 14; Page 55; 106pp; English.
XX
AAT48210-25 are att recombination site core region DNA sequences. The
CC core region has at least one engineered mutation that enhances
CC recombination in vitro in the formation of a Cointegrate or Product DNA.
CC These core regions can be incorporated into novel vector donor DNA
CC molecules. The nucleic acids, vectors and methods of the invention are
CC used to obtain chimeric nucleic acid using recombination proteins and
CC engineered recombination sites in vitro or in vivo. The improved
CC specificity, speed and yields of the invention facilitates DNA or RNA
CC subcloning, regulation or exchange useful for any related purpose, e.g.
CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
CC or modification of transcribed, replicated, isolated or genomic DNA or
CC RNA
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SQ Sequence 25 BP; 4 A; 5 C; 4 G; 6 T; 0 U; 6 Other;

Query Match      78.4%; Score 19.6; DB 2; Length 25;
Best Local Similarity 80.0%; Pred. No. 12;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTYYKTRTACNAASTSGB 25
   ::|||:|||||:|||||:|||||
Db 1 AGCCWGCTTTCRTACNAAGTSGB 25

RESULT 4
AAT48214
ID AAT48214 standard; DNA; 25 BP.
XX
AC AAT48214;
XX
DT 20-OCT-1997 (first entry)
XX
DE M-attP1 core region.
XX
att recombination site; core region; mutation; enhance; recombination;
KW vector; subcloning; regulation; exchange; ss.
XX
```


OS Synthetic.
 XX WO9640724-A1.
 PN 19-DEC-1996.
 XX 07-JUN-1996; 96WO-US010082.
 XX 07-JUN-1995; 95US-00486139.
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 XX Hartley JL, Brasch MA;
 XX WPI; 1997-065168/06.
 DR Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
 XX using recombinant proteins and engineered recombination sites in vitro or
 PT in vivo.
 XX Claim 14; Page 55; 106pp; English.
 XX AAT48210-25 are att recombination site core region DNA sequences. The
 CC core region has at least one engineered mutation that enhances
 CC recombination in vitro in the formation of a Cointegrate or Product DNA.
 CC These core regions can be incorporated into novel vector donor DNA
 CC molecules. The nucleic acids, vectors and methods of the invention are
 CC used to obtain chimeric nucleic acid using recombination proteins and
 CC engineered recombination sites in vitro or in vivo. The improved
 CC specificity, speed and yields of the invention facilitates DNA or RNA
 CC subcloning, regulation or exchange useful for any related purpose, e.g.
 CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
 CC or modification of transcribed, replicated, isolated or genomic DNA or
 CC RNA
 XX Sequence 25 BP; 4 A; 3 C; 4 G; 8 T; 0 U; 6 Other;
 PS Claim 14; Page 55; 106pp; English.
 XX AAT48210-25 are att recombination site core region DNA sequences. The
 CC core region has at least one engineered mutation that enhances
 CC recombination in vitro in the formation of a Cointegrate or Product DNA.
 CC These core regions can be incorporated into novel vector donor DNA
 CC molecules. The nucleic acids, vectors and methods of the invention are
 CC used to obtain chimeric nucleic acid using recombination proteins and
 CC engineered recombination sites in vitro or in vivo. The improved
 CC specificity, speed and yields of the invention facilitates DNA or RNA
 CC subcloning, regulation or exchange useful for any related purpose, e.g.
 CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
 CC or modification of transcribed, replicated, isolated or genomic DNA or
 CC RNA
 XX Sequence 25 BP; 4 A; 3 C; 4 G; 8 T; 0 U; 6 Other;
 SQ Query Match 78.4%; Score 19.6; DB 2; Length 25;
 Best Local Similarity 80.0%; Pred. No. 12;
 Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RKYCWGCTTYYKTRTACNAAGTSGB 25
 Db 1 GTTCAGCTTYYKTRTACNAAGTSGB 25
 RESULT 5
 AAT48211
 ID AAT48211 standard; DNA; 25 BP.
 XX AAT48211;
 XX 20-OCT-1997 (first entry)
 DT M-attB core region.
 XX att recombination site; core region; mutation; enhance; recombination;
 XX vector; subcloning; regulation; exchange; ss.
 XX Synthetic.
 XX WO9640724-A1.
 XX 19-DEC-1996.
 XX 07-JUN-1996; 96WO-US010082.
 XX 07-JUN-1995; 95US-00486139.
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 XX Hartley JL, Brasch MA;
 XX WPI; 1997-065168/06.
 DR Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
 XX using recombinant proteins and engineered recombination sites in vitro or
 PT in vivo.
 XX Claim 14; Page 55; 106pp; English.
 XX AAT48210-25 are att recombination site core region DNA sequences. The
 CC core region has at least one engineered mutation that enhances
 CC recombination in vitro in the formation of a Cointegrate or Product DNA.
 CC These core regions can be incorporated into novel vector donor DNA
 CC molecules. The nucleic acids, vectors and methods of the invention are
 CC used to obtain chimeric nucleic acid using recombination proteins and
 CC engineered recombination sites in vitro or in vivo. The improved
 CC specificity, speed and yields of the invention facilitates DNA or RNA
 CC subcloning, regulation or exchange useful for any related purpose, e.g.
 CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
 CC or modification of transcribed, replicated, isolated or genomic DNA or
 CC RNA
 XX Sequence 25 BP; 4 A; 3 C; 4 G; 8 T; 0 U; 6 Other;
 PS Claim 14; Page 55; 106pp; English.
 XX AAT48210-25 are att recombination site core region DNA sequences. The
 CC core region has at least one engineered mutation that enhances
 CC recombination in vitro in the formation of a Cointegrate or Product DNA.
 CC These core regions can be incorporated into novel vector donor DNA
 CC molecules. The nucleic acids, vectors and methods of the invention are
 CC used to obtain chimeric nucleic acid using recombination proteins and
 CC engineered recombination sites in vitro or in vivo. The improved
 CC specificity, speed and yields of the invention facilitates DNA or RNA
 CC subcloning, regulation or exchange useful for any related purpose, e.g.
 CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
 CC or modification of transcribed, replicated, isolated or genomic DNA or
 CC RNA
 XX Sequence 25 BP; 4 A; 3 C; 4 G; 8 T; 0 U; 6 Other;
 SQ Query Match 78.4%; Score 19.6; DB 2; Length 25;
 Best Local Similarity 84.0%; Pred. No. 12;
 Matches 21; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RKYCWGCTTYYKTRTACNAAGTSGB 25
 Db 1 AGCCWGCCTTYYKTRTACNAAGTSGB 25
 RESULT 6
 AAX78938
 ID AAX78938 standard; DNA; 25 BP.
 XX AAX78938;
 XX 17-AUG-1999 (first entry)
 DT Oligonucleotide #4 for recombination and cloning method.
 XX Cloning; donor; recombination site; vector; chimeric; ss.
 XX Synthetic.
 XX WO9921977-A1.
 XX 06-MAY-1999.
 XX 26-OCT-1998; 98WO-US022589.
 XX 24-OCT-1997; 97US-0065930P.
 XX 23-OCT-1998; 98US-00177387.
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 XX Hartley JL, Brasch MA, Temple GF, Fox DK;
 XX WPI; 1999-303011/25.
 XX New nucleic acid cloning methods.
 XX Disclosure; Page 159; 185pp; English.
 XX The invention relates to novel methods for cloning or subcloning one or
 CC more nucleic acid molecules (NAME) comprising: (a) combining in vitro or
 CC in vivo: (i) at least one insert donor molecules (IDMs) comprising one or
 CC more desired nucleic acid segments flanked by at least 2 recombination
 CC sites which do not recombine with each other; (2) one or more vector
 CC donor molecules (VDMs) comprising at least 2 recombination sites which do
 CC not recombine with each other; and (3) one or more site-specific
 CC recombination proteins; (b) incubating the combination to transfer one or

more of the desired segments into one or more of the VDMs, thereby producing one or more desired product molecules (PMs). The methods can be used for the efficient and specific recombination of NAM segments. They can be used to generate chimeric DNA or RNA molecules that have the desired characteristics and/or nucleic acid segments. The methods can also be used for changing vectors. The oligonucleotides AAX78935-X78994 are used in the method of the invention.

Q Sequence 25 BP; 4 A; 5 C; 4 G; 6 T; 0 U; 6 Other;

Query Match 78.4%; Score 19.6; DB 2; Length 25;
Best Local Similarity 80.0%; Pred. No. 12;
Matches 20; Conservative 5; Mismatches 0;
Indels 0; Gaps 0;

Qy	1	RKYCWGCTT	YKTRTACNA	ASTSGB	25
	:	:	:	:	:
D _b	1	AGCCWGCTT	CKTRTACNA	AGTSGB	25

RESULT 7
AAX78945
ID AAX78945 standard: DNA: 25 BP.

AC AAX78945;

DT 17-AUG-1999 (first entry)

DE Oligonucleotide #11 for recombination and cloning method.

KW Cloning; donor; recombination site; vector; chimeric; ss.

OS Synthetic.

PN WO9921977-A1.

PD 06-MAY-1999.

PF 26-OCT-1998; 98WO-US022589.

PR 24-OCT-1997; 97US-0065930P.

XX

XX

XX

XX XX

XX

more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or in vivo: (1) at least one insert donor molecules (IDMs) comprising one or more desired nucleic acid segments flanked by at least 2 recombination sites which do not recombine with each other; (2) one or more vector donor molecules (VDMs) comprising at least 2 recombination sites which do not recombine with each other; and (3) one or more site-specific recombination proteins; (b) incubating the combination to transfer one or more of the desired segments into one or more of the VDMs, thereby producing one or more desired product molecules (PMS). The methods can be used for the efficient and specific recombination of NAM segments. They can be used to generate chimeric DNA or RNA molecules that have the desired characteristics and/or nucleic acid segments. The methods can also be used for changing vectors. The oligonucleotides AAX78935-X78994 are used in the method of the invention.

SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 U; 0 Other;

Query Match 78.4%; Score 19.6; DB 2; Length 25;
Best Local Similarity 56.0%; Pred. No. 12;
Matches 14; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy

1 RKYCWGCTTTTKTRTACNAASTGB 25
:::|:::|:::|:::|:::|:::|:::

Db

1 GTTCAGCTTCTTGTAACAAGTGGT 25

RESULT 8
AAX78936
ID AAX78936 standard: DNA; 25 BP.

AC AAX78936:

DT 17-AUG-1999 (first entry)

DE Oligonucleotide #2 for recombination and cloning method.

KW Cloning; donor; recombination site; vector; chimeric; ss.

OS Synthetic.

PN WO9921977-A1.

PD 06-MAY-1999.

PF 26-OCT-1998; 98WO-US022589.

PR 24-OCT-1997; 97US-0065930P.

XXXXXX

XX XX

XX

XX

XX

XX

more nucleic acid molecules (NAMs) comprising: (a) combining *in vitro* or *in vivo*: (1) at least one insert donor molecules (IDWs) comprising one or more desired nucleic acid segments flanked by at least 2 recombination sites which do not recombine with each other; (2) one or more vector donor molecules (VDMs) comprising at least 2 recombination sites which do not recombine with each other; and (3) one or more site-specific recombination proteins; (b) incubating the combination to transfer one or more of the desired segments into one or more of the VDMs, thereby producing one or more desired product molecules (PMs). The methods can be used for the efficient and specific recombination of NAM segments. They can be used to generate chimeric DNA or RNA molecules that have the desired characteristics and/or nucleic acid segments. The methods can also be used for changing vectors. The oligonucleotides AAX78935-X78994 are used in the method of the invention.

Sequence 25 BP: 4 A; 5 C; 3 G; 6 T; 0 U; 7 Other;

Query Match	78.4%	Score 19.6;	DB 2;	Length 25;
Best Local Similarity	84.0%;	Pred. No. 12;		
Matches 21: Conservative		4; Mismatches	0; Indels	0; Gaps

Qy	1	RKYCWGCTTTTYKTRTACNAASTSGB	25
	:	:	:
D_b	1	AGCCWGCTTTTYKTRTACNAACTSGB	25

RESULT 9
AAX78974
ID AAX78974 standard; DNA; 25 BP.

AC AAX78974;

DT 17-AUG-1999 (first entry)

CC The invention relates to novel methods for cloning or subcloning one or
CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
CC more desired nucleic acid segments flanked by at least 2 recombination
CC sites which do not recombine with each other; (2) one or more vector
CC donor molecules (VDMs) comprising at least 2 recombination sites which do
CC not recombine with each other; and (3) one or more site-specific
CC recombination proteins; (b) incubating the combination to transfer one or
CC more of the desired segments into one or more of the VDMs, thereby
CC producing one or more desired product molecules (PMs). The methods can be
CC used for the efficient and specific recombination of NAM segments. They
CC can be used to generate chimeric DNA or RNA molecules that have the
CC desired characteristics and/or nucleic acid segments. The methods can
CC also be used for changing vectors. The oligonucleotides AAX78935-X78994
CC are used in the method of the invention

SQ Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 5 Other;

Query Match 78.4%; Score 19.6; DB 2; Length 25;
Best Local Similarity 76.0%; Pred. No. 12;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTYYKTRTACNAASTSG 25
Db 1 GTTCAGCTTCKTRTACNAASTSG 25

RESULT 12

AAX78935
ID AAX78935 standard; DNA; 25 BP.

XX AC AAX78935;

XX DT 17-AUG-1999 (first entry)

XX DE Oligonucleotide #1 for recombination and cloning method.

XX KW Cloning; donor; recombination site; vector; chimeric; ss.

XX OS Synthetic.

XX PN WO9921977-A1.

XX PD 06-MAY-1999.

XX PF 26-OCT-1998; 98WO-US022589.

XX PR 24-OCT-1997; 97US-0065930P.

XX PR 23-OCT-1998; 98US-00177387.

XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Hartley JL, Brasch MA, Temple GF, Fox DK;

XX PR WPI; 1999-303011/25.

XX PT New nucleic acid cloning methods.

XX PS Disclosure; Page 158; 185pp; English.

XX CC The invention relates to novel methods for cloning or subcloning one or
XX more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
XX in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
XX more desired nucleic acid segments flanked by at least 2 recombination
XX sites which do not recombine with each other; (2) one or more vector
XX donor molecules (VDMs) comprising at least 2 recombination sites which do
XX not recombine with each other; and (3) one or more site-specific
XX recombination proteins; (b) incubating the combination to transfer one or
XX more of the desired segments into one or more of the VDMs, thereby
XX producing one or more desired product molecules (PMs). The methods can be
XX used for the efficient and specific recombination of NAM segments. They
XX can be used to generate chimeric DNA or RNA molecules that have the
XX desired characteristics and/or nucleic acid segments. The methods can

CC also be used for changing vectors. The oligonucleotides AAX78935-X78994
CC are used in the method of the invention

SQ Sequence 25 BP; 3 A; 3 C; 2 G; 6 T; 0 U; 11 Other;

Query Match 78.4%; Score 19.6; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTYYKTRTACNAASTSG 25
Db 1 RKYCWGCTTYYKTRTACNAASTSG 25

RESULT 13

AAX78939
ID AAX78939 standard; DNA; 25 BP.

XX AC AAX78939;

XX DT 17-AUG-1999 (first entry)

XX DE Oligonucleotide #5 for recombination and cloning method.

XX KW Cloning; donor; recombination site; vector; chimeric; ss.

XX OS Synthetic.

XX PN WO9921977-A1.

XX PD 06-MAY-1999.

XX PF 26-OCT-1998; 98WO-US022589.

XX PR 24-OCT-1997; 97US-0065930P.

XX PR 23-OCT-1998; 98US-00177387.

XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Hartley JL, Brasch MA, Temple GF, Fox DK;

XX PR WPI; 1999-303011/25.

XX PT New nucleic acid cloning methods.

XX PS Disclosure; Page 159; 185pp; English.

XX CC The invention relates to novel methods for cloning or subcloning one or
XX more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
XX in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
XX more desired nucleic acid segments flanked by at least 2 recombination
XX sites which do not recombine with each other; (2) one or more vector
XX donor molecules (VDMs) comprising at least 2 recombination sites which do
XX not recombine with each other; and (3) one or more site-specific
XX recombination proteins; (b) incubating the combination to transfer one or
XX more of the desired segments into one or more of the VDMs, thereby
XX producing one or more desired product molecules (PMs). The methods can be
XX used for the efficient and specific recombination of NAM segments. They
XX can be used to generate chimeric DNA or RNA molecules that have the
XX desired characteristics and/or nucleic acid segments. The methods can
XX also be used for changing vectors. The oligonucleotides AAX78935-X78994
XX are used in the method of the invention

SQ Sequence 25 BP; 4 A; 3 C; 4 G; 8 T; 0 U; 6 Other;

Query Match 78.4%; Score 19.6; DB 2; Length 25;
Best Local Similarity 80.0%; Pred. No. 12;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTYYKTRTACNAASTSG 25
Db 1 GTTCAGCTTYYKTRTACNAAGTSG 25

```
RESULT 14
AAS06185
ID AAS06185 standard; DNA; 25 BP.
XX
AC AAS06185;
XX
DT 12-SEP-2001 (first entry)
XX
DE Phage-lambda recombination site attR2.
XX
KW Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
KW lambda integrase; therapeutic; ss.
XX
OS Bacteriophage lambda.
XX
PN WO200142509-A1.
XX
PD 14-JUN-2001.
XX
PF 11-DEC-2000; 2000WO-US033546.
XX
PR 10-DEC-1999; 99US-0169983P.
PR 09-MAR-2000; 2000US-0188020P.
XX
PA (CHEO/) CHEO D.
PA (BRAS/) BRASCH M A.
PA (TEMP/) TEMPLE G F.
PA (HART/) HARTLEY J L.
PA (BYRD/) BYRD D R N.
XX
PI Cheo D, Brasch MA, Temple GF, Hartley JL, Byrd DRN;
XX
DR WPI; 2001-356174/37.
XX
PT Producing hybrid nucleic acids, useful for expressing novel therapeutic
PT polypeptides, by mixing the same or different nucleic acids having one or
PT more recombination sites in the presence of recombination proteins, e.g.
PT Cre.
XX
PS Disclosure; Fig 24A; 357pp; English.
XX
CC AAS06174-AAS06322 represent Bacteriophage lambda att recombination site
CC nucleic acid sequences, and PCR primers of the invention. The att
CC sequences are recognised by the recombination protein lambda integrase
CC (Int). The invention is a new method of producing a population of hybrid
CC nucleic acids comprising mixing at least a first population of nucleic
CC acids comprising one or more recombination sites with at least one target
CC nucleic acid comprising one or more recombination sites and causing some
CC or all of the nucleic acids to recombine with all or some of the target
CC nucleic acids. The method is useful for producing a population of hybrid
CC nucleic acids which may be the same or different. The nucleic acids may
CC be used to express therapeutic proteins or peptides and they may also be
CC used to create novel fusion proteins by expressing different sequences
CC linked to each other. The method allows simultaneous cloning of two or
CC more different nucleic acids
XX
SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 U; 0 Other;
Query Match 78.4%; Score 19.6; DB 4; Length 25;
Best Local Similarity 56.0%; Pred. No. 12;
Matches 14; Conservative 10; Mismatches 1; Indels 0; Gaps 0;
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DB 1 GTTCAGCTTCTTGTAACAAAGTGGT 25
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Job time : 168.8 secs

RESULT 15
AAC87867
ID AAC87867 standard; DNA; 25 BP.
XX
AC AAC87867;
XX
DT 02-MAR-2001 (first entry)
XX
DE Escherichia coli core region recombinant site m-attB SEQ ID NO:2.
XX
KW Core region; recombination site; cloning; chimeric DNA; characteristic;
KW mutation; att site; lox site; ss.
XX
OS Escherichia coli.
XX
PN US6143557-A.
XX
PD 07-NOV-2000.
XX
PF 20-JAN-1999; 99US-00233493.
XX
PR 07-JUN-1995; 95US-00486139.
PR 07-JUN-1996; 96US-00663002.
PR 12-JAN-1998; 98US-00005476.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Brasch MA, Hartley JL;
XX
DR WPI; 2001-049004/06.
XX
PT Isolated nucleic acid molecules comprising a DNA segment having two
PT engineered recombination sites, derived from att or lox, which flank a
PT selectable marker and comprise a core region having an engineered
PT mutation.
XX
PS Claim 1; Col 18; 73pp; English.
XX
CC The present invention describes an isolated nucleic acid molecule (I)
CC comprising a first nucleic acid sequence having a defined sequence
CC (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,
CC or an RNA sequence corresponding to AAC87866 to AAC87881. Also described
CC are: (1) an isolated nucleic acid molecule (II) comprising a first
CC mutated recombination site that removes one or more stop codons from the
CC recombination site or avoids hairpin formation, the recombination site
CC being an att or lox site; (2) an isolated nucleic acid molecule (III)
CC comprising a first att recombination site comprising a mutation that
CC enhances recombination specificity; (3) vectors (IV) comprising the above
CC mentioned nucleic acids; and (4) cells comprising the above mentioned
CC nucleic acids or (IV). The nucleic acids are used in engineering a core
CC region of a given recombination site to provide mutative sites suitable
CC for subcloning reactions. The use of nucleic acids for obtaining
CC engineered recombination in vitro or in vivo makes the methods for DNA or
CC RNA subcloning, highly specific, rapid, and less labour intensive
XX
SQ Sequence 25 BP; 4 A; 5 C; 3 G; 6 T; 0 U; 7 Other;
Query Match 78.4%; Score 19.6; DB 4; Length 25;
Best Local Similarity 84.0%; Pred. No. 12;
Matches 21; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 RKYCWGCTTYYKTRTACNAASTSGB 25
DB 1 AGCGWGTCTTYKTRTACNAACTSGB 25
Search completed: November 16, 2004, 04:02:44
Job time : 168.8 secs
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:19 ; Search time 35.9 Seconds
(without alignments)
494.978 Million cell updates/sec

Title: US-10-820-133-1

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	19.6	78.4	25	3	US-09-233-493-3
4	19.6	78.4	25	3	US-09-233-493-4
5	19.6	78.4	25	3	US-09-233-493-5
6	19.6	78.4	25	3	US-09-233-493-6
7	19.6	78.4	25	3	US-09-005-476-1
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16	19.6	78.4	25	3	US-09-296-280-1
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36 19.6 78.4 25 5 PCT-US96-10082A-3
37 19.6 78.4 25 5 PCT-US96-10082A-4
38 19.6 78.4 25 5 PCT-US96-10082A-5
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ALIGNMENTS

RESULT 1
US-09-233-493-1
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; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
US-09-233-493-1

CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-493-4

Query Match 78.4%; Score 19.6; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCGCTTYYKTRTACNAASTSG 25
Db 1 AGCCGCTTCTCKTRTACNAAGTSG 25

RESULT 5
US-09-233-493-5
Sequence 5, Application US/09233493
Patent No. 6143557
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-493-5

Query Match 78.4%; Score 19.6; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCGCTTYYKTRTACNAASTSG 25
Db 1 GTTCAGCTTYYKTRTACNAAGTSG 25

RESULT 6
US-09-005-476-1
Sequence 1, Application US/09005476
Patent No. 6171861
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,476
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-005-476-1

Query Match 78.4%; Score 19.6; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCGCTTYYKTRTACNAASTSG 25

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Db      1 RKYCWGCTTYKTRTACNAASTSGB 25

RESULT 7
; Sequence 2, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; US-09-005-476-2

Query Match      78.4%; Score 19.6; DB 3; Length 25;
Best Local Similarity 84.0%; Pred. No. 1.2;
Matches 21; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RKYCWGCTTYKTRTACNAASTSGB 25
      ::::::::::::::::::::
Db      1 AGCCWGCTTYKTRTACNAACTSGB 25

RESULT 8
; Sequence 3, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; US-09-005-476-4

Query Match      78.4%; Score 19.6; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.2;
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; US-09-005-476-3

Query Match      78.4%; Score 19.6; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.2;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RKYCWGCTTYKTRTACNAASTSGB 25
      ::::::::::::::::::::
Db      1 GTTCAGCTTCTKTRTACNAACTSGB 25

RESULT 9
US-09-005-476-4
; Sequence 4, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; US-09-005-476-4

Query Match      78.4%; Score 19.6; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.2;
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Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTYYKTRTACNAASTSGB 25
Db 1 AGCCWGCCTTCKTRTACNAAGTSGB 25

RESULT 10
US-09-005-476-5
; Sequence 5, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005.476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-005-476-5

Query Match 78.4%; Score 19.6; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTYYKTRTACNAASTSGB 25
Db 1 GTTCAGCTTYYKTRTACNAAGTSGB 25

RESULT 11
US-09-233-492-1
; Sequence 1, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA

; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233.492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663.002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486.139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-233-492-1

Query Match 78.4%; Score 19.6; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTYYKTRTACNAASTSGB 25
Db 1 RKYCWGCTTYYKTRTACNAASTSGB 25

RESULT 12
US-09-233-492-2
; Sequence 2, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233.492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663.002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486.139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-492-2

Query Match 78.4%; Score 19.6; DB 3; Length 25;
Best Local Similarity 84.0%; Pred. No. 1.2;
Matches 21; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTCTKTRTACNAAGTSG 25
Db 1 AGCCWGCCTTCTKTRTACNAAGTSG 25

RESULT 13
US-09-233-492-3
Sequence 3, Application US/092333492
Patent No. 6270969
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-492-3

Query Match 78.4%; Score 19.6; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.2;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTCTKTRTACNAAGTSG 25
Db 1 AGCCWGCCTTCTKTRTACNAAGTSG 25

Db 1 GTTCAGCTTCTKTRTACNAAGTSG 25

RESULT 14
US-09-233-492-4
Sequence 4, Application US/092333492
Patent No. 6270969
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-492-4

Query Match 78.4%; Score 19.6; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTCTKTRTACNAAGTSG 25
Db 1 AGCCWGCCTTCTKTRTACNAAGTSG 25

RESULT 15
US-09-233-492-5
Sequence 5, Application US/092333492
Patent No. 6270969
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-492-5

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; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-233-492-5

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Query Match      78.4%; Score 19.6; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. NO. 1.2;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RKYCWGCTTYKTRTACNAAGTSG 25
   ::::|||||:|||||:|||||
Db 1 GTTACGCTTYKTRTACNAAGTSG 25

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Search completed: November 16, 2004, 10:22:29
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:34:49 : Search time 314 Seconds
(without alignments)
430.015 Million cell updates/sec

Title: US-10-820-133-1

Perfect score: 25

Sequence: 1 rkycwgcttttyktrtacnaastsgb 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
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- 18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	19.6	78.4	25	9	US-09-732-914-12
2	19.6	78.4	25	9	US-09-855-797A-1
3	19.6	78.4	25	9	US-09-855-797A-2
4	19.6	78.4	25	9	US-09-855-797A-3
5	19.6	78.4	25	9	US-09-855-797A-4
6	19.6	78.4	25	9	US-09-855-797A-5
7	19.6	78.4	25	9	US-09-855-797A-11
8	19.6	78.4	25	9	US-09-855-797A-40
9	19.6	78.4	25	9	US-09-855-797A-42
10	19.6	78.4	25	9	US-09-822-634-4
11	19.6	78.4	25	9	US-09-822-634-5
12	19.6	78.4	25	9	US-09-907-900-1

13	19.6	78.4	25	9	US-09-907-900-2	Sequence 2, Appli
14	19.6	78.4	25	9	US-09-907-900-3	Sequence 3, Appli
15	19.6	78.4	25	9	US-09-907-900-4	Sequence 4, Appli
16	19.6	78.4	25	9	US-09-907-900-5	Sequence 5, Appli
17	19.6	78.4	25	9	US-09-907-900-11	Sequence 11, Appli
18	19.6	78.4	25	9	US-09-907-900-40	Sequence 40, Appli
19	19.6	78.4	25	9	US-09-907-900-42	Sequence 42, Appli
20	19.6	78.4	25	9	US-09-907-719-1	Sequence 1, Appli
21	19.6	78.4	25	9	US-09-907-719-2	Sequence 2, Appli
22	19.6	78.4	25	9	US-09-907-719-3	Sequence 3, Appli
23	19.6	78.4	25	9	US-09-907-719-4	Sequence 4, Appli
24	19.6	78.4	25	9	US-09-907-719-5	Sequence 5, Appli
25	19.6	78.4	25	9	US-09-907-719-11	Sequence 11, Appli
26	19.6	78.4	25	9	US-09-907-719-40	Sequence 40, Appli
27	19.6	78.4	25	9	US-09-907-719-42	Sequence 42, Appli
28	19.6	78.4	25	10	US-09-432-085-1	Sequence 1, Appli
29	19.6	78.4	25	10	US-09-432-085-2	Sequence 2, Appli
30	19.6	78.4	25	10	US-09-432-085-3	Sequence 3, Appli
31	19.6	78.4	25	10	US-09-432-085-4	Sequence 4, Appli
32	19.6	78.4	25	10	US-09-432-085-5	Sequence 5, Appli
33	19.6	78.4	25	10	US-09-985-448-1	Sequence 1, Appli
34	19.6	78.4	25	10	US-09-985-448-2	Sequence 2, Appli
35	19.6	78.4	25	10	US-09-985-448-3	Sequence 3, Appli
36	19.6	78.4	25	10	US-09-985-448-4	Sequence 4, Appli
37	19.6	78.4	25	10	US-09-985-448-5	Sequence 5, Appli
38	19.6	78.4	25	10	US-09-985-448-11	Sequence 11, Appli
39	19.6	78.4	25	10	US-09-985-448-40	Sequence 40, Appli
40	19.6	78.4	25	10	US-09-985-448-42	Sequence 42, Appli
41	19.6	78.4	25	14	US-10-058-292-1	Sequence 1, Appli
42	19.6	78.4	25	14	US-10-058-292-2	Sequence 2, Appli
43	19.6	78.4	25	14	US-10-058-292-3	Sequence 3, Appli
44	19.6	78.4	25	14	US-10-058-292-4	Sequence 4, Appli
45	19.6	78.4	25	14	US-10-058-292-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-732-914-12
; Sequence 12, Application US/09732914
; Patent No. US20020007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in
; TITLE OF INVENTION: Recombinational Cloning
; FILE REFERENCE: 0942.5010002
; CURRENT APPLICATION NUMBER: US/09/732.914
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 25
; TYPE: DNA
; ORGANISM: attr2
US-09-732-914-12

Query Match 78.4%; Score 19.6; DB 9; Length 25;
Best Local Similarity 56.0%; Pred. No. 9.2;
Matches 14; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTTTYKTRTACNAASTSGB 25

Db 1 GTTCAGCTTCTTGTCACAAAGTGT 25

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RESULT 2
US-09-855-797A-1
; Sequence 1, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855.797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-1

Query Match          78.4%; Score 19.6; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTYYKTRTACNAASTSG 25
Db 1 RKYCWGCTTYYKTRTACNAASTSG 25

RESULT 3
US-09-855-797A-2
; Sequence 2, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855.797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-2

Query Match          78.4%; Score 19.6; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTYYKTRTACNAASTSG 25
Db 1 RKYCWGCTTYYKTRTACNAASTSG 25
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Query Match          78.4%; Score 19.6; DB 9; Length 25;
Best Local Similarity 84.0%; Pred. No. 9.2;
Matches 21; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTYYKTRTACNAASTSG 25
Db 1 AGCCWGCTTYYKTRTACNAACTSG 25

RESULT 4
US-09-855-797A-3
; Sequence 3, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855.797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-3

Query Match          78.4%; Score 19.6; DB 9; Length 25;
Best Local Similarity 76.0%; Pred. No. 9.2;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTYYKTRTACNAASTSG 25
Db 1 GTTCAGCTTTCRTACNAACTSG 25

RESULT 5
US-09-855-797A-4
; Sequence 4, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855.797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 25
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; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-4

Query Match          78.4%; Score 19.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 9.2;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTTTKRTACNAASTSGB 25
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Db 1 AGCCWGCCTTCTKTRTACNAAGTSGB 25

RESULT 6
US-09-855-797A-5
; Sequence 5, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-5

Query Match          78.4%; Score 19.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 9.2;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTTTKRTACNAASTSGB 25
   ::::::::::::::::::::::::::::::
Db 1 GTTCAGCTTTTKRTACNAAGTSGB 25

RESULT 7
US-09-855-797A-11
; Sequence 11, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
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; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-11

Query Match          78.4%; Score 19.6; DB 9; Length 25;
Best Local Similarity 56.0%; Pred. No. 9.2;
Matches 14; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTTTKRTACNAASTSGB 25
   ::::::::::::::::::::::::::::
Db 1 GTTCAGCTTTCTGTACAAAGTGCT 25

RESULT 8
US-09-855-797A-40
; Sequence 40, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-40

Query Match          78.4%; Score 19.6; DB 9; Length 25;
Best Local Similarity 72.0%; Pred. No. 9.2;
Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTTTKRTACNAASTSGB 25
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Db 1 ASCCWGCTTTTTRTACWAASTRGW 25

RESULT 9
US-09-855-797A-42
; Sequence 42, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
```

; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-42

Query Match 78.4%; Score 19.6; DB 9; Length 25;
Best Local Similarity 68.0%; Pred. No. 9.2;
Matches 17; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTTTKTRTACNAASTSG 25
:::|||||:|||||:|||||:|||||:
Db 1 GTTCAGCTTTTKTRTACWAATSGW 25

RESULT 10
US-09-822-634-4
; Sequence 4, Application US/09822634
; Patent No. US20020150556A1
; GENERAL INFORMATION:
; APPLICANT: Vile, Richard G.
; APPLICANT: Harrington, Kevin
; APPLICANT: Bateman, Andrew
; APPLICANT: Murphy, Steven
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TISSUE
; TITLE OF INVENTION: SPECIFIC GENE REGULATION THERAPY
; FILE REFERENCE: 07039-289001
; CURRENT APPLICATION NUMBER: US/09/822,634
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/193,977
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated vector sequence
; NAME/KEY: misc.feature
; LOCATION: (1)...(25)
; OTHER INFORMATION: n = A,T,C or G
US-09-822-634-4

Query Match 78.4%; Score 19.6; DB 9; Length 25;
Best Local Similarity 76.0%; Pred. No. 9.2;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTTTKTRTACNAASTSG 25
:::|||||:|||||:|||||:|||||:
Db 1 GTTCAGCTTTTKTRTACNAACTSG 25

RESULT 11
US-09-822-634-5
; Sequence 5, Application US/09822634
; Patent No. US20020150556A1
; GENERAL INFORMATION:
; APPLICANT: Vile, Richard G.
; APPLICANT: Harrington, Kevin

; APPLICANT: Bateman, Andrew
; APPLICANT: Murphy, Steven
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TISSUE
; TITLE OF INVENTION: SPECIFIC GENE REGULATION THERAPY
; FILE REFERENCE: 07039-289001
; CURRENT APPLICATION NUMBER: US/09/822,634
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/193,977
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated vector sequence
; NAME/KEY: misc.feature
; LOCATION: (1)...(25)
; OTHER INFORMATION: n = A,T,C or G
US-09-822-634-5

Query Match 78.4%; Score 19.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 9.2;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTTTKTRTACNAASTSG 25
:::|||||:|||||:|||||:|||||:
Db 1 AGCCWGGCTTTCKTRTACNAAGTSG 25

RESULT 12
US-09-907-900-1
; Sequence 1, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-1

Query Match 78.4%; Score 19.6; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTTTKTRTACNAASTSG 25
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Db 1 RKYCWGCTTTTKTRTACNAASTSG 25

RESULT 13
US-09-907-900-2
; Sequence 2, Application US/09907900

; Patent No. US20020172997A1

; GENERAL INFORMATION:

; APPLICANT: Hartley, James L.

; APPLICANT: Brasch, Michael A.

; APPLICANT: Temple, Gary F.

; APPLICANT: Fox, Donna K.

; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites

; FILE REFERENCE: 0942.2850004

; CURRENT APPLICATION NUMBER: US/09/907,900

; CURRENT FILING DATE: 2001-07-19

; PRIOR APPLICATION NUMBER: 09/177,387

; PRIOR FILING DATE: 1998-10-23

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Unknown

; FEATURE:

; NAME/KEY: OTHER

; LOCATION: 18

; OTHER INFORMATION: "n" may be any nucleotide

; OTHER INFORMATION: Description of Unknown Organism: recombination

; OTHER INFORMATION: products

US-09-907-900-2

Query Match

Best Local Similarity 78.4%; Score 19.6; DB 9; Length 25;

Matches 21; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTYYKTRTACNAASTSGB 25

Db 1 AGCCWGCCTTYYKTRTACNAACTSGB 25

:::|||||:|||||:|||||:|||||

RESULT 14

US-09-907-900-3

; Sequence 3, Application US/09907900

; Patent No. US20020172997A1

; GENERAL INFORMATION:

; APPLICANT: Hartley, James L.

; APPLICANT: Brasch, Michael A.

; APPLICANT: Temple, Gary F.

; APPLICANT: Fox, Donna K.

; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites

; FILE REFERENCE: 0942.2850004

; CURRENT APPLICATION NUMBER: US/09/907,900

; CURRENT FILING DATE: 2001-07-19

; PRIOR APPLICATION NUMBER: 09/177,387

; PRIOR FILING DATE: 1998-10-23

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Unknown

; FEATURE:

; NAME/KEY: OTHER

; LOCATION: 18

; OTHER INFORMATION: "n" may be any nucleotide

; OTHER INFORMATION: Description of Unknown Organism: recombination

; OTHER INFORMATION: products

US-09-907-900-3

Query Match

Best Local Similarity 78.4%; Score 19.6; DB 9; Length 25;

Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTYYKTRTACNAASTSGB 25

Db 1 GTTCAGCTTCTCKTRTACNAACTSGB 25

:::|||||:|||||:|||||:|||||

RESULT 15

US-09-907-900-4

; Sequence 4, Application US/09907900

; Patent No. US20020172997A1

; GENERAL INFORMATION:

; APPLICANT: Hartley, James L.

; APPLICANT: Brasch, Michael A.

; APPLICANT: Temple, Gary F.

; APPLICANT: Fox, Donna K.

; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites

; FILE REFERENCE: 0942.2850004

; CURRENT APPLICATION NUMBER: US/09/907,900

; CURRENT FILING DATE: 2001-07-19

; PRIOR APPLICATION NUMBER: 09/177,387

; PRIOR FILING DATE: 1998-10-23

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Unknown

; FEATURE:

; NAME/KEY: OTHER

; LOCATION: 18

; OTHER INFORMATION: "n" may be any nucleotide

; OTHER INFORMATION: Description of Unknown Organism: recombination

; OTHER INFORMATION: products

US-09-907-900-4

Query Match

Best Local Similarity 78.4%; Score 19.6; DB 9; Length 25;

Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTYYKTRTACNAASTSGB 25

Db 1 AGCCWGCCTTCTCKTRTACNAAGTSGB 25

:::|||||:|||||:|||||:|||||

Search completed: November 16, 2004, 11:14:57

Job time : 314.1 secs

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:04 ; Search time 1532 Seconds
(without alignments)
594.643 Million cell updates/sec

Title: US-10-820-133-1

Perfect score: 25

Sequence: 1 rkywgttttyktrtaacnaastgb 25

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821986598 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gsl1:*

9: gb_gsl2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19.6	78.4	321	2	BF086649 CM0-BN007
2	19.6	78.4	595	2	AW993039 RC2-BN003
3	19.6	78.4	635	7	CN484020 hw41b03.Y
C 4	19.6	78.4	672	8	AQ990864 Rfc01701
5	19.6	78.4	706	4	B1836912 603084230
6	19.6	78.4	714	5	BX359053 BX359053
7	19.6	78.4	752	4	BG620766 602617479
C 8	19.6	78.4	753	8	AQ990861 Rfc01698
9	19.6	78.4	797	4	BG427603 602497040
10	19.6	78.4	805	7	CF629462 DKFZP469K
C 11	19.6	78.4	808	8	AQ990388 Rfc01153
12	19.6	78.4	810	5	BQ216337 AGENCOURT
13	19.6	78.4	824	4	BG620383 602617507
14	19.6	78.4	831	5	BQ230007 AGENCOURT
15	19.6	78.4	852	4	BG401996 602466712
16	19.6	78.4	855	2	BE785867 601478671
17	19.6	78.4	856	2	BE893159 601437059
18	19.6	78.4	859	5	BX398237 BX398237
19	19.6	78.4	862	2	BE895530 601438319
20	19.6	78.4	888	7	CK209237 FGAS02099
21	19.6	78.4	908	4	BT546971 603190186
22	19.6	78.4	954	5	BQ893686 AGENCOURT
23	19.6	78.4	986	5	BX398580 BX398580
24	19.6	78.4	994	4	BM804936 AGENCOURT

25	19.6	78.4	994	7	CK162659
26	19.6	78.4	1012	7	CK211630
27	19.6	78.4	1019	2	BE300319
28	19.6	78.4	1031	7	CK163965
29	19.6	78.4	1031	7	CK212789
30	19.6	78.4	1043	7	CK212830
31	19.6	78.4	1051	7	CK212815
32	19.6	78.4	1053	7	CK212320
33	19.6	78.4	1059	7	CK163940
34	19.6	78.4	1062	7	CK212429
35	19.6	78.4	1067	7	CK212431
36	19.6	78.4	1070	7	CK2113073
37	19.6	78.4	1071	7	CK211886
38	19.6	78.4	1071	7	CK212465
39	19.6	78.4	1076	7	CK216054
40	19.6	78.4	1076	7	CK217224
41	19.6	78.4	1082	7	CK212170
42	19.6	78.4	1088	7	CK205724
43	19.6	78.4	1093	7	CK211774
44	19.6	78.4	1095	7	CK212335
45	19.6	78.4	1098	7	CK213245

ALIGNMENTS

RESULT 1
BF086649/c

LOCUS BF086649 321 bp mRNA linear EST 19-OCT-2000
DEFINITION CM0-GN0077-160900-559-g06 GN0077 Homo sapiens CDNA, mRNA sequence.

ACCESSION BF086649

VERSION BF086649.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 321)

AUTHORS Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P.,

Goldman, G.H., Carvalho, A.P., Mateukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2=CM0-GN0077-160

900-559-g06&tl=32000-09-16&tl=1)

Seq primer: puc 18 forward

High quality sequence start: 12

High quality sequence stop: 321.

FEATURES

source

1. 321

/location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="GN0077"

/notes="Organ: placenta_normal; Vector: puc18; Site: 1:

SmaI; Site 2: SmaI; A mini-library was made by cloning

products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

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Query Match      78.4%; Score 19.6; DB 2; Length 321;
Best Local Similarity 56.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY      1  RKYCWGCTTTTKRTACNAASTGGB 25

Db      186  GTTCTGCTTTCTTATACCAAGTGGC 162

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RESULT 2	AW993039	595 bp	linear	EST 05-JUN-2000
LOCUS	RC2-BN0033-060200-012-c06	BN0033	Homo sapiens	cdNA, mRNA sequence.
DEFINITION	AW993039			
ACCESSION	AW993039.1	GI:8253175		
VERSION				
KEYWORDS	EST.			

homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1. (bases 1 to 595)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brundstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
 O'Hate, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.

TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202663
PUBMED	10737800
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

FEATURES

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BN0033"
/note="Organ: breast normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

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ORIGIN

Query Match	78.4%	Score 19.6;	DB 2;	Length 595;
Best Local Similarity	56.0%;	Pred. No. 1.4e+02;		
Matches 14: Conservative	10;	Mismatches 1;	Indels 0;	Gaps 0;

QY 1 RKYCWGCTTYYKTRTACNAASTSGB 25
:::|||||:::|||||:::|:
Db 88 GTTCTGCTTCTTATACCAAGTGGC 112

RESULT 3
CN484020

CN484020 635 bp mRNA linear EST 26-APR-2004
hw41b03.y2 Human primary human ocular pericytes. Unamplified (hw)
Homo sapiens cDNA clone hw41b03 5', mRNA sequence.
CN484020
CN484020.1 GI:46565524
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 635)
Tsai, J. Y. and Wistow, G.

JOURNAL
COMMENT

CONTENTS

ORIGIN

```
Query Match      78.4%; Score 19.6; DB 7; Length 635;
Best Local Similarity 56.0%; Pred.No. 1.5e+02;
Matches 14: Conservative 10; Mismatches 1; Indels 0; Gaps 0;
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RESULT 4
AO990864/C

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VERSION      AQ990864.1  GI:9649458
KEYWORDS     GSS.
SOURCE       Photorhabdus luminescens
ORGANISM     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
              Enterobacteriaceae; Photorhabdus.
REFERENCE    1 (bases 1 to 672)
AUTHORS      french-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
              Daborn,P.O., Bowen,B. and Blactner,F.R.
TITLE        A genomic sample sequence of the entomopathogenic bacterium
              Photorhabdus luminescens W14: potential implications for virulence
JOURNAL      Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
MEDLINE      20378633
PUBMED       10319786
COMMENT      Contact: french-Constant RH
              Department of Biology and Biochemistry
              University of Bath
              South Building, Bath BA2 7AY, UK
              Tel: (44) 1225 826621
              Fax: (44) 1225 826779
              Email: bsrf@bath.ac.uk
              This is one of 2,122 random reads from the M13 library. For
              annotation of identified clones (BLASTX, BLASTN and mapping to E.
              coli K12 genome) please see french-Constant et al. 2000, Nucleic
              Acids Res.
              Seq primer: M13 Forward
              Class: shotgun.
FEATURES     source
              Location/Qualifiers
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                /organism="Photorhabdus luminescens"
                /mol_type="genomic DNA"
                /strain="W14"
                /db_xref="taxon:29488"
                /clone="PLG01701"
                /dev_stage="Primary phase variant"
                /clone_lib="Photorhabdus luminescens strain W14 M13
                library"
                /note="Genomic DNA from strain W14 was size selected (1-2
                kb) and then cloned into M13 Janus."
ORIGIN
              Query Match      78.4%; Score 19.6; DB 8; Length 672;
              Best Local Similarity 56.0%; Pred. No. 1.5e+02;
              Matches 14; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RKYCGCTTTTKRTACNAASTSGB 25
    ::::::::::::::::::::
Db 637 GTTCAGCTTTTATCTACTAGTGC 613

RESULT 5
BI836912
LOCUS      BI836912
DEFINITION 603084230F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5223318 5',
              mRNA sequence.
ACCESSION  BI836912
VERSION     BI836912.1  GI:15948462
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 706)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabbs-remail.nih.gov
              Tissue Procurement: Life Technologies, Inc.
              cDNA Library Preparation: Life Technologies, Inc.
              DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be

```

```

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM1561 row: 1 column: 07
High quality sequence stop: 646.
Location/Qualifiers
  1..706
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clones="IMAGE:5223318"
  /lab_host="DH10B"
  /clone_lib="NIH_MGC_120"
  /note="Organ: pooled pancreas and spleen; Vector:
  pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
  source anonymous pool of spleen and pancreas from 28 yo
  male. Library is oligo-dT primed and directionally cloned
  (EcoRV site is destroyed upon cloning). Average insert
  size 1.5 kb, insert size range 1-2.5 kb. Library is
  normalized and enriched for full-length clones and was
  constructed by C. Gruber (Invitrogen). Research Genetics
  tracking code 025. Note: this is a NIH_MGC Library."
ORIGIN
              Query Match      78.4%; Score 19.6; DB 4; Length 706;
              Best Local Similarity 56.0%; Pred. No. 1.5e+02;
              Matches 14; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RKYCGCTTTTKRTACNAASTSGB 25
    ::::::::::::::::::::
Db 269 GTTCTGCTTCTTATACCAAGTGC 293

RESULT 6
BX359053
LOCUS      BX359053
DEFINITION BX359053 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
              clone CSODI052YG13 5-PRIME, mRNA sequence.
ACCESSION  BX359053
VERSION     BX359053.2  GI:46291338
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 714)
AUTHORS      Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE        Full-length cDNA libraries and normalization
JOURNAL      Unpublished (2001)
COMMENT      On May 5, 2003 this sequence version replaced gi:30372318.
              Contact: Genoscope
              Genoscope - Centre National de Sequencage
              BP 191 91006 EVRY cedex - France
              Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
              1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
              end enriched, double-strand cDNA was digested with Not I and cloned
              into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
              was normalized. Library was constructed by Life Technologies, a
              division of Invitrogen. This sequence belongs to sequence cluster
              470.x
              For more information about this cluster, see
              http://www.genoscope.cns.fr/cdna/s=CSODI052AD07QPI&c=470.r.
              Location/Qualifiers
                1..714
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="CSODI052YG13"
                /tissue="PLACENTA COT 25-NORMALIZED"
                /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                /note="1st strand cDNA was primed with a NotI-oligo(dT)
                primer. Five prime end enriched, double-strand cDNA was
                digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
FEATURES     source
              Location/Qualifiers
                1..714
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                /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                /note="1st strand cDNA was primed with a NotI-oligo(dT)
                primer. Five prime end enriched, double-strand cDNA was
                digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

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DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MCC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1CM1356 row: p column: 10
 High quality sequence stop: 703.
 Location/Qualifiers

FEATURES

source

1..797
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="IMAGE:4610937"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site:1:
 SfiI (ggccattatggcc); Site:2: SfiI (ggccattatggcc); 5' and
 3' adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CAGCGCATTATGCGC-3' and 3' adaptor sequence:
 5'-ATTCTAGGCGCGAGCGCGGCACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.65
 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MCC Library."

ORIGIN

Query Match 78.4%; Score 19.6; DB 4; Length 797;
 Best Local Similarity 56.0%; Pred. No. 1.5e+02;
 Matches 14; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTYYKTRTACNAASTSG 25

Db 429 GTTCTGCTTTCTTATACCAAGTGGC 453
 :::::::::::|||||

RESULT 10

CR629462 805 bp mRNA linear EST 11-AUG-2004
 LOCUS DKFPZ469K1521_r1_469 (synonym: pkid1) Pongo pygmaeus cDNA clone
 DEFINITION DKFPZ469K1521_5', mRNA sequence.

ACCESSION CR629462

VERSION CR629462.1 GI:51125542

KEYWORDS EST.

SOURCE Pongo pygmaeus (orangutan)

ORGANISM

Pongo pygmaeus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.

1 (bases 1 to 805)

Bahr, A., Lauber, J., Mewes, H.W., Weil, B., Aml, C., Osanger, A.,

Fobo, G., Han, M. and Wiemann, S.

Pongo pygmaeus mRNA (Bahr, A., Lauber, J., Mewes, H.W., et al.)

Unpublished (2004)

Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert from S. Wiemann,
 Molecular Genome Analysis, German Cancer Research Center (DKFZ);
 Email s.wiemann@dkfz-heidelberg.de; sequenced by Qiagen
 (Hilden/Germany) within the cDNA sequencing consortium of the
 German Genome Project. This clone (DKFPZ469K1521) is available at
 the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
 Berlin, Germany. Please contact RZPD for ordering:
<http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFPZ469K1521>
 Further information about the clone and the sequencing project is
 available at <http://mips.gsf.de/projects/cdna/>.

FEATURES

source

1..805
 /organism="Pongo pygmaeus"
 /mol_type="mRNA"
 /db_xref="taxon:9600"
 /clone="DKFPZ469K1521"
 /tissue_type="kidney"
 /dev_stage="adult"

ORIGIN
 Query Match 78.4%; Score 19.6; DB 7; Length 805;
 Best Local Similarity 56.0%; Pred. No. 1.5e+02;
 Matches 14; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RKYCWGCTTYYKTRTACNAASTSG 25

Db 543 GTTCTGCTTTCTTATACCAAGTGGC 567
 :::::::::::|||||

RESULT 11

AQ990388/c

LOCUS

DEFINITION

AQ990388

KEYWORDS

GSS.

SOURCE

ORGANISM

Photorhabdus luminescens

Photorhabdus luminescens

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Enterobacteriaceae; Photorhabdus.

1 (bases 1 to 808)

ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,

Daborn, P.J., Bowen, D. and Blattner, F.R.

A genomic sample sequence of the entomopathogenic bacterium

Photorhabdus luminescens W14: potential implications for virulence

Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

20378633

10919786

Contact: ffrench-Constant RH

Department of Biology and Biochemistry

University of Bath

South Building, Bath BA2 7AY, UK

Tel: (44) 1225 826621

Fax: (44) 1225 826779

Email: bsr@bath.ac.uk

This is one of 2,122 random reads from the M13 library. For

annotation of identified clones (BLASTX, BLASTN and mapping to E.

coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic

Acids Res.

Seq primer: M13 Forward

Class: shotgun.

Location/Qualifiers

1..808

/organism="Photorhabdus luminescens"

/mol_type="genomic DNA"

/strain="W14"

/db_xref="taxon:29488"

/clone="PLG01153"

/dev_stage="primary phase variant"

/clone_lib="Photorhabdus luminescens strain W14 M13

library"

/note="Genomic DNA from strain W14 was size selected (1-2

kb) and then cloned into M13 Janus."

ORIGIN

Query Match

Best Local Similarity

Matches

14; Conservative

10; Mismatches

1; Indels

0; Gaps

0;

Qy

1 RKYCWGCTTYYKTRTACNAASTSG 25

Db

628 GTTCAGCTTTTATACCAAGTGGC 604

:::|||||

RESULT 12

BQ216337


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Query Match      78.4%; Score 19.6; DB 5; Length 831;
Best Local Similarity 56.0%; Pred. No. 1.5e+02;
Matches 14; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKYCWGCTTYYKTRTACNAASTGB 25
      : : : : : : : : : : : : : : : :
DB 567 GTTCTGCTTCTTATACCAAGTGC 591
      : : : : : : : : : : : : : : : :

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RESULT 15	BG401996	852 bp	mRNA	linear	EST 12-MAR-2001			
LOCUS	602466712F1	NIH_MGC_75	Homo sapiens	CDNA clone	IMAGE:4594610 5',			
DEFINITION	mRNA sequence.							
ACCESSION	BG401996							
VERSION	BG401996.1	GI:13295444						
KEYWORDS	EST.							
SOURCE	Homo sapiens (human)							
ORGANISM	Homo sapiens							
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
	1 (bases 1 to 852)							
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/ .							
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)							
TITLE	Unpublished (1999)							
JOURNAL	Contact: Robert Strausberg, Ph.D.							
COMMENT	Email: cgabbs@mail.nih.gov							
	Tissue Procurement: CLONTECH Laboratories, Inc.							
	CDNA Library Preparation: CLONTECH Laboratories, Inc.							
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)							
	DNA Sequencing by: Incyte Genomics, Inc.							
	Clone distribution: MGC clone distribution information can be							
	found through the I.M.A.G.E. Consortium/LLNL at:							
	http://image.llnl.gov							
	Plate: LLCM1336 row: h column: 03							
	High quality sequence stop: 591.							

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1. 852
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4594610"
/lab_host="DH10B (T1 phage-resistant)"
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/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggcgctatggcc); Site_2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCATATGGCC-3', 3' adaptor sequence: 5'-ATTCTAGAGCCGCGCGGCACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH MGC Library."

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Query Match      78.4%; Score 19.6; DB 4; Length 852;
Best Local Similarity 56.0%; Pred. No. 1.5e+02;
Matches 14; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY   1 RKYCWGCTTYYTKRTACNAASTGSB 25
Db    409 GTTCGTCTTTCTATACCAAGTGSC 433
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Search completed: November 16, 2004, 10:16:27
Job time : 1536 secs

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Db      1 AGCCWGCCTTYYKTRTACNAACTSGB 25

RESULT 5
AX498612
LOCUS   AX498612
DEFINITION
Sequence 2 from Patent EP1229113.
ACCESSION
AX498612
VERSION
AX498612.1 GI:23343409
KEYWORDS
SOURCE
ORGANISM
.
unidentified
unidentified
unclassified.

REFERENCE
1 Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
TITLE
Patent: EP 1229113-A 2 07-AUG-2002;
JOURNAL
INVITROGEN CORPORATION (US)

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1..25
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Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AGCCWGCCTTYYKTRTACNAACTSGB 25
|||||
1 AGCCWGCCTTYYKTRTACNAACTSGB 25

Db      1 AGCCWGCCTTYYKTRTACNAACTSGB 25

RESULT 6
BD131328
LOCUS   BD131328
DEFINITION
Recombinational cloning using nucleic acids having recombination
sites.
ACCESSION
BD131328
VERSION
BD131328.1 GI:23226273
KEYWORDS
JP 2002500861-A/2.
SOURCE
unidentified
ORGANISM
unclassified.

REFERENCE
1 (bases 1 to 25)
Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
Recombinational cloning using nucleic acids having recombination
TITLE
Patent: JP 2002500861-A 2 15-JAN-2002;
JOURNAL
LIFE TECHNOLOGIES INC

COMMENT
OS Unknown
PN JP 2002500861-A/2
PD 15-JAN-2002
PF 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930, 23-OCT-1998 US 09/177387 PI
JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC
C12N15/09, C12Q1/68, C12N15/00
CC Description of Unknown Organism: recombination products FH
Key Description of Unknown Organisms
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 84.8%; Score 21.2; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AGCCWGCCTTYYKTRTACNAACTSGB 25

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5994. .6120
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6145. .6210
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6211. .6264
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6296. .6505
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11226. .11334
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Best Local Similarity 72.0%; Pred. No. 7.8;
Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

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RESULT 8
AC118378/c AC118378 256498 bp DNA linear HTG 11-OCT-2002
LOCUS

DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Rattus norvegicus clone CH230-35816, *** SEQUENCING IN PROGRESS
***, 2 unordered pieces.
AC118378
AC118378.4 GI:23618102
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 256498)
Muzny,D.,Marie., Metzker,M.,Lee., Abramson,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Aryalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,S.,
Fernandez,S., Finley,M., Flegg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Gaszta,M.,
Gebregregis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Haves,A., Henderson,N., Hernandez,J.,
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Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
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Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
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Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
Valas,R., Vera,V., Villaseana,D., Waldron,L., Walker,B., Wang,J.,
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Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 256498)
Worley,K.C.
Direct Submission
Submitted (17-APR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 256498)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (11-OCT-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

On Oct 9, 2002 this sequence version replaced gi:21746207.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GYIC
Center clone name: CH230-35816
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 183400 bases at least Q40
Consensus quality: 186096 bases at least Q30
Consensus quality: 187794 bases at least Q20
Estimated insert size: 190483; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
consists of 2 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

* 1 255030: contig of 255030 bp in length
* 255031 255130: gap of unknown length
* 255131 255498: contig of 1368 bp in length.

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/db_xref="taxon:10116"
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1. 1782
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7744..8660
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Query Match 84.8%; Score 21.2; DB 2; Length 256498;
Best Local Similarity 72.0%; Pred. No. 7.8;
Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGCCGCGCTTTCRTACAACTGCB 25
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RESULT 9
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LOCUS
DEFINITION Rattus norvegicus clone CH230-74A9, *** SEQUENCING IN PROGRESS ***,
4 unordered pieces.
AC121737
VERSION AC121737.4 GI:25138094
HTG: HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 263259)
Muzny,D,Maric, Metzker,M, Lee, Abramzon, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
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Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
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Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
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Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G. and Gibbs, R.A.

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TITLE JOURNAL
REFERENCE JOURNAL
AUTHORS JOURNAL
TITLE JOURNAL
JOURNAL
REFERENCE JOURNAL
AUTHORS JOURNAL
TITLE JOURNAL
JOURNAL
COMMENT
FEATURES
source
misc_feature
misc_feature
misc_feature
ORIGIN

```

Direct Submission
Unpublished
2 (bases 1 to 263259)
Worley, K.C.
Direct Submission
Submitted (21-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 263259)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 20, 2002 this sequence version replaced gi:22856055.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GVVJ
Center clone name: CH230-74A9
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 233743 bases at least Q40
Consensus quality: 237630 bases at least Q30
Consensus quality: 239718 bases at least Q20
Estimated insert size: 239635; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 257713: contig of 257713 bp in length
* 257714 257813: gap of unknown length
* 257814 258996: contig of 1183 bp in length
* 258997 259096: gap of unknown length
* 259097 261187: contig of 2091 bp in length
* 261188 261287: gap of unknown length
* 261288 263259: contig of 1972 bp in length.
Location/Qualifiers
1..263259
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-74A9"
1..1068
/note="wgs contig"
2206..5186
/note="wgs contig"
256153..257713
/note="wgs_contig"

Query Match 84.8%; Score 21.2; DB 2; Length 263259;
Best Local Similarity 72.0%; Pred. No. 7.8;
Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
Qy 1 AGCCGCTTYYKRTACNAACTSGB 25
||||:||||:||||:||||:||||:||||:
Db 156871 AGCCTGCTTCTTATACAACTGGG 156895

RESULT 10
AC123037 137122 bp DNA linear ROD 01-JAN-2004
DEFINITION Mus musculus BAC clone RP24-527F14 from chromosome 6, complete sequence.
AC123037
AC123037.4 GI:38229487
VERSION HTG.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 137122)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Tin-Wollam, A., Cotton, M. and Boyer, E.
JOURNAL The sequence of Mus musculus BAC clone RP24-527F14
REFERENCE 2 (bases 1 to 137122)
AUTHORS Unpublished (2001)
TITLE Sequencing of Mus musculus
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 137122)
AUTHORS McPherson, J.D. and Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (27-MAY-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 4 (bases 1 to 137122)
AUTHORS Wilson, R.K.
TITLE Direct Submission
JOURNAL Submitted (22-OCT-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 5 (bases 1 to 137122)
AUTHORS Wilson, R.K.
TITLE Direct Submission
JOURNAL Submitted (08-NOV-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 6 (bases 1 to 137122)
AUTHORS Wilson, R.
TITLE Direct Submission
JOURNAL Submitted (01-JAN-2004) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT On Nov 8, 2003 this sequence version replaced gi:37806531.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: submissions@wustl.edu
----- Summary Statistics

Center project name: M_B0527F14

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

Db 86972 AGCGTCTTCTTATACAACTGG 86995

RESULT 11
AC147382 198872 bp DNA linear PRI 19-MAY-2004
LOCUS Pan troglodytes BAC clone RP43-171M24 from 7, complete sequence.
DEFINITION AC147382
ACCESSION AC147382
VERSION AC147382.3 GI:45736892
KEYWORDS HTG.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
TITLE 1 (bases 1 to 198872)
JOURNAL The sequence of Pan troglodytes BAC clone RP43-171M24
AUTHORS Shah, N., Bielicki, L. and Haglund, K.
TITLE Unpublished (2001)
JOURNAL 2 (bases 1 to 198872)
AUTHORS Wilson, R.K.
TITLE Direct Submission
JOURNAL Submitted (11-NOV-2003) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 3 (bases 1 to 198872)
AUTHORS Wilson, R.K.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-2004) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 4 (bases 1 to 198872)
AUTHORS Wilson, R.K.
TITLE Direct Submission
JOURNAL Submitted (25-MAR-2004) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 5 (bases 1 to 198872)
AUTHORS Wilson, R.K.
TITLE Direct Submission
JOURNAL Submitted (19-MAY-2004) Washington University School of Medicine,
Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO
63108, USA
COMMENT On Mar 25, 2004 this sequence version replaced gi:42734583.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu>
Contact: submissions@watson.wustl.edu
----- Summary Statistics
Center project name: C_Pt171M24

NOTICE:

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. Wes Warren,
Department of Genetics, Washington University, St. Louis MO. For
additional information about the map position of this sequence, see
<http://genome.wustl.edu>

SOURCE INFORMATION:
The RPCI-43 BAC library has been constructed by Chung-Li Shu. DNA
was isolated from white blood cells obtained from a male chimpanzee
(Pan troglodytes, 'Clint', Yerkes #C0471, birthdate: 6-6-80). The
clone and detailed information can be obtained from ResGen
(<http://www.resgen.com>) or Pieter de Jong and co-workers at
<http://www.bacpac.chori.org>.

NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone. This clone is
overlapped by AC146098.
Location/Qualifiers
1..198872
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/chromosome="7"
/map="7"
/clone="RP43-171M24"
/clone_lib="RPCI-43"

ORIGIN
Query Match 84.0%; Score 21; DB 9; Length 198872;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 18; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Oy 1 AGCCGCTTTTCTTACNAACTSG 24
|||||:|||||:|||||:|||||
Db 63546 AGCCAGCTTTGTATACCACTGG 63569
|||||:|||||:|||||:|||||

RESULT 12
AC125159/c
LOCUS AC125159 204431 bp DNA linear HTG 25-AUG-2002
DEFINITION Mus musculus chromosome UNK clone RP24-394C23, WORKING DRAFT
SEQUENCE, 8 unordered pieces.
ACCESSION AC125159
VERSION AC125159.3 GI:22476252
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 204431)
AUTHORS McPherson, J.D. and Waterston, R.H.
TITLE The sequence of Mus musculus clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 204431)
AUTHORS McPherson, J.D. and Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (20-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
REFERENCE 3 (bases 1 to 204431)
AUTHORS McPherson, J.D. and Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (25-AUG-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
COMMENT On Aug 25, 2002 this sequence version replaced gi:22002221.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc/index.shtml>
Contact: submissions@watson.wustl.edu
----- Project Information
Center project name: M_BB0394C23

----- Summary Statistics
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 201646 bases at least Q40
Consensus quality: 202298 bases at least Q30
Consensus quality: 202670 bases at least Q20
Insert size: 139000; agarose-fp
Insert size: 203731; sum-of-contigs
Quality coverage: 13.99 in Q20 bases; agarose-fp
Quality coverage: 11.84 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 3397: contig of 3397 bp in length
 3398 3497: gap of unknown length
 3498 11345: contig of 7848 bp in length
 11346 11445: gap of unknown length
 11446 33842: contig of 22397 bp in length
 33843 33942: gap of unknown length
 33943 63612: contig of 29670 bp in length
 63613 63712: gap of unknown length
 63713 91001: contig of 27289 bp in length
 91002 91101: gap of unknown length
 91102 123616: contig of 32515 bp in length
 123617 123716: gap of unknown length
 123717 162626: contig of 38910 bp in length
 162627 162726: gap of unknown length
 162727 204431: contig of 41705 bp in length.

FEATURES

source
 1..204431
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /chromosome="UNK"
 /clone="RP24-394C23"
 misc_feature
 1..3397
 /note="assembly_name:Contig12"
 misc_feature
 3498..11345
 /note="assembly_name:Contig13"
 misc_feature
 11446..33842
 /note="assembly_name:Contig14"
 misc_feature
 33943..63612
 /note="assembly_name:Contig15"
 misc_feature
 63713..91001
 /note="assembly_name:Contig16"
 misc_feature
 91102..123616
 /note="assembly_name:Contig17"
 misc_feature
 123717..162626
 /note="assembly_name:Contig18"
 misc_feature
 162727..204431
 /note="assembly_name:Contig19"

ORIGIN

Query Match 84.0%; Score 21; DB 2; Length 204431;
 Best Local Similarity 75.0%; Pred. No. 10;
 Matches 18; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGCCGCTTYYKTRTACNACTSG 24

Db 56693 AGCCTGCTTCTTATACAACTGG 56670

RESULT 13

BD131366 BD131366 25 bp DNA linear PAT 18-SEP-2002
 LOCUS Recombinational cloning using nucleic acids having recombination sites.

ACCESSION BD131366
 VERSION BD131366.1 GI:23226311
 KEYWORDS JP 2002500861-A/40.
 SOURCE unidentified
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 25)
 AUTHORS Hartley, J.L., Brasch, M.A., Temple, G.F. and Fox, D.K.
 TITLE Recombinational cloning using nucleic acids having recombination sites
 JOURNAL Patent: JP 2002500861-A 40 15-JAN-2002;
 LIFE TECHNOLOGIES INC

COMMENT

OS Unknown
 PN JP 2002500861-A/40
 PD 15-JAN-2002
 PF 26-OCT-1998 JP 2000518069
 PR 24-OCT-1997 US 60/065930, 23-OCT-1998 US 09/177387 PI
 JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC
 C12N15/09, C12Q1/68, C12N15/00
 CC Description of Unknown Organism: recombination products FH

Key source Location/Qualifiers

FT source 1..25
 /organism="Unknown".

FEATURES

source
 1..25
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

ORIGIN

Query Match 81.6%; Score 20.4; DB 6; Length 25;
 Best Local Similarity 76.0%; Pred. No. 30;
 Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGCCGCTTYYKTRTACNACTSG 25

Db 1 ASCCGCTTYYTFTACAACTG 25

RESULT 14

AR124526 AR124526 25 bp DNA linear PAT 16-MAY-2001
 LOCUS Sequence 6 from patent US 6171861.
 DEFINITION AR124526
 ACCESSION AR124526
 VERSION AR124526.1 GI:14109887
 KEYWORDS

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 25)

AUTHORS Hartley, J.L. and Brasch, M.A.
 TITLE Recombinational cloning using engineered recombination sites
 JOURNAL Patent: US 6171861-A 6 09-JAN-2001;
 FEATURES Location/Qualifiers

source

1..25
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 80.0%; Score 20; DB 6; Length 25;
 Best Local Similarity 72.0%; Pred. No. 48;
 Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCCGCTTYYKTRTACNACTSG 25

Db 1 AGCCTGCTTYYTGTACAACTGT 25

RESULT 15

AR124527 AR124527 25 bp DNA linear PAT 16-MAY-2001
 LOCUS Sequence 7 from patent US 6171861.
 DEFINITION AR124527
 ACCESSION AR124527
 VERSION AR124527.1 GI:14109889
 KEYWORDS

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 25)

AUTHORS Hartley, J.L. and Brasch, M.A.
 TITLE Recombinational cloning using engineered recombination sites
 JOURNAL Patent: US 6171861-A 7 09-JAN-2001;
 FEATURES Location/Qualifiers

source

1..25
 /organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 80.0%; Score 20; DB 6; Length 25;
Best Local Similarity 72.0%; Pred. No. 48;
Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGCCWGCCTTYKRTACNAACTSGE 25
|||:|||||:|:|:|:|:|:|:|:|:
Db 1 AGCCTGCTTTCTTGACAACTGT 25

Search completed: November 16, 2004, 06:00:59
Job time : 710.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:29:13 ; Search time 167.8 Seconds
(without alignments)
782.095 Million cell updates/sec

Title: US-10-820-133-2

Perfect score: 25

Sequence: 1 agcwgcttcttctacnaactsqb 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134896 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_23Sep04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21.2	84.8	25	2	AAT48211
2	21.2	84.8	25	2	AAX78936
3	21.2	84.8	25	4	AAC87867
4	21.2	84.8	25	4	AAF55736
5	21.2	84.8	25	4	AAD14430
6	21.2	84.8	25	8	ABT16622
7	21.2	84.8	25	9	ACD28277
8	21.2	84.8	25	9	ACD28477
9	21.2	84.8	25	9	ADA38163
10	21.2	84.8	25	10	AAD60559
11	21.2	84.8	25	10	ACC44651
12	21.2	84.8	25	12	ADL93417
13	20.4	81.6	25	2	AAX78974
14	20	80.0	25	2	AAT48216
15	20	80.0	25	2	AAT48215
16	20	80.0	25	2	AAX78940
17	20	80.0	25	2	AAX78941
18	20	80.0	25	3	AAC55380
19	20	80.0	25	4	AAS06178
20	20	80.0	25	4	AAC87899
21	20	80.0	25	4	AAC87898

ALIGNMENTS

RESULT 1

AAT48211
ID AAT48211 standard; DNA; 25 BP.

XX AC AAT48211;

XX DT 20-OCT-1997 (first entry)

XX DE M-attB core region.

XX KW att recombination site; core region; mutation; enhance; recombination; vector; subcloning; regulation; exchange; ss.

XX OS Synthetic.

XX PN WO9640724-A1.

XX PD 19-DEC-1996.

XX PF 07-JUN-1996; 96WO-US010082.

XX PR 07-JUN-1995; 95US-00486139.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Hartley JL, Brasch MA;

XX WPI; 1997-065168/06.

XX PT Nucleic acids, vectors and methods to obtain chimeric nucleic acid - using recombinant proteins and engineered recombination sites in vitro or in vivo.

XX PS Claim 14; Page 55; 106pp; English.

XX CC AAT48210-25 are att recombination site core region DNA sequences. The core region has at least one engineered mutation that enhances recombination in vitro in the formation of a Cointegrate or Product DNA. These core regions can be incorporated into novel vector donor DNA molecules. The nucleic acids, vectors and methods of the invention are used to obtain chimeric nucleic acid using recombination proteins and engineered recombination sites in vitro or in vivo. The improved specificity, speed and yields of the invention facilitates DNA or RNA subcloning, regulation or exchange useful for any related purpose, e.g.

Aac87872 Escherich
Aac87871 Escherich
Aaf55740 Recombina
Aaf55767 PCR prime
Aaf55768 PCR prime
Aaf55741 Recombina
Aaf55741 ATT gite
Aad14434 Recombina
Aad14435 Recombina
Abq82118 Core sequ
Abq82119 Core sequ
Abt16626 Artificia
Acd28428 Engineere
Acd28281 Nucleic a
Acd28282 Nucleic a
Acd28429 Engineere
Acd28481 Nucleic a
Acd28482 Nucleic a
Acd28607 Engineere
Acd28608 Engineere
Ada38195 Complemen
Ada38194 Complemen
Ada38167 DNA of a
Ada38168 DNA of a

22 20 80.0 25 4 AAC87872
23 20 80.0 25 4 AAC87871
24 20 80.0 25 4 AAF55740
25 20 80.0 25 4 AAF55767
26 20 80.0 25 4 AAF55768
27 20 80.0 25 4 AAF55741
28 20 80.0 25 4 AAF55741
29 20 80.0 25 4 AAD14434
30 20 80.0 25 4 AAD14435
31 20 80.0 25 6 ABQ82118
32 20 80.0 25 6 ABQ82119
33 20 80.0 25 8 ABT16626
34 20 80.0 25 9 ACD28428
35 20 80.0 25 9 ACD28281
36 20 80.0 25 9 ACD28282
37 20 80.0 25 9 ACD28429
38 20 80.0 25 9 ACD28481
39 20 80.0 25 9 ACD28482
40 20 80.0 25 9 ACD28607
41 20 80.0 25 9 ACD28608
42 20 80.0 25 9 ADA38195
43 20 80.0 25 9 ADA38194
44 20 80.0 25 9 ADA38167
45 20 80.0 25 9 ADA38168

CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
CC or modification of transcribed, replicated, isolated or genomic DNA or
CC RNA

SQ Sequence 25 BP; 4 A; 5 C; 3 G; 6 T; 0 U; 7 Other;

Query Match 84.8%; Score 21.2; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCGCTTTTKTRTACNAACTSGB 25
Db 1 AGCCGCTTTTKTRTACNAACTSGB 25

RESULT 2

AA78936
ID AAX78936 standard; DNA; 25 BP.

AC AAX78936;

XX 17-AUG-1999 (first entry)

XX Oligonucleotide #2 for recombination and cloning method.

XX Cloning; donor; recombination site; vector; chimeric; ss.

XX Synthetic.

XX WO9921977-A1.

XX 06-MAY-1999.

XX 26-OCT-1998; 98WO-US022589.

XX 24-OCT-1997; 97US-0065930P.

XX 23-OCT-1998; 98US-00177387.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Fox DK;

XX WPI; 1999-303011/25.

XX New nucleic acid cloning methods.

XX Disclosure; Page 159, 185pp; English.

CC The invention relates to novel methods for cloning or subcloning one or
CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
CC more desired nucleic acid segments flanked by at least 2 recombination
CC sites which do not recombine with each other; (2) one or more vector
CC donor molecules (VDMs) comprising at least 2 recombination sites which do
CC not recombine with each other; and (3) one or more site-specific
CC recombination proteins; (b) incubating the combination to transfer one or
CC more of the desired segments into one or more of the VDMs, thereby
CC producing one or more desired product molecules (PMs). The methods can be
CC used for the efficient and specific recombination of NAM segments. They
CC can be used to generate chimeric DNA or RNA molecules that have the
CC desired characteristics and/or nucleic acid segments. The methods can
CC also be used for changing vectors. The oligonucleotides AAX78935-X78994
CC are used in the method of the invention

SQ Sequence 25 BP; 4 A; 5 C; 3 G; 6 T; 0 U; 7 Other;

Query Match 84.8%; Score 21.2; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCGCTTTTKTRTACNAACTSGB 25
Db 1 AGCCGCTTTTKTRTACNAACTSGB 25

RESULT 3

AAC87867

ID AAC87867 standard; DNA; 25 BP.

XX AAC87867;

XX 02-MAR-2001 (first entry)

XX Escherichia coli core region recombinant site m-attB SEQ ID NO:2.

XX Core region; recombination site; cloning; chimeric DNA; characteristic;
XX mutation; att site; lox site; ss.

XX Escherichia coli.

XX US6143557-A.

XX 07-NOV-2000.

XX 20-JAN-1999; 99US-00233493.

XX 07-JUN-1995; 95US-00486139.

XX 07-JUN-1996; 96US-00663002.

XX 12-JAN-1998; 98US-00005476.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Brasch MA, Hartley JL;

XX WPI; 2001-049004/06.

XX Isolated nucleic acid molecules comprising a DNA segment having two
XX engineered recombination sites, derived from att or lox, which flank a
XX selectable marker and comprise a core region having an engineered
XX mutation.

XX Claim 1; Col 18; 73pp; English.

XX The present invention describes an isolated nucleic acid molecule (I)
XX comprising a first nucleic acid sequence having a defined sequence
XX (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,
XX or an RNA sequence corresponding to AAC87866 to AAC87881. Also described
XX are: (1) an isolated nucleic acid molecule (II) comprising a first
XX mutated recombination site that removes one or more stop codons from the
XX recombination site or avoids hairpin formation, the recombination site
XX being an att or lox site; (2) an isolated nucleic acid molecule (III)
XX comprising a first att recombination site comprising a mutation that
XX enhances recombination specificity; (3) vectors (IV) comprising the above
XX mentioned nucleic acids; and (4) cells comprising the above mentioned
XX nucleic acids or (IV). The nucleic acids are used in engineering a core
XX region of a given recombination site to provide mutative sites suitable
XX for subcloning reactions. The use of nucleic acids for obtaining
XX engineered recombination in vitro or in vivo makes the methods for DNA or
XX RNA subcloning, highly specific, rapid, and less labour intensive

SQ Sequence 25 BP; 4 A; 5 C; 3 G; 6 T; 0 U; 7 Other;

Query Match 84.8%; Score 21.2; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCGCTTTTKTRTACNAACTSGB 25
Db 1 AGCCGCTTTTKTRTACNAACTSGB 25

RESULT 4

AAF55736

ID AAF55736 standard; DNA; 25 BP.

XX AAF55736;


```

XX 12-APR-2001 (first entry)
XX DT
XX DE
XX REcombination site m-attB.
XX KW
XX OS
XX Unidentified.
XX OS
XX US6171861-B1.
XX PN
XX 09-JAN-2001.
XX PD
XX 12-JAN-1998; 98US-00005476.
XX PF
XX 07-JUN-1995; 95US-00486139.
XX PR
XX 07-JUN-1996; 96US-00663002.
XX PA
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX PI
XX Hartley JL, Brasch MA;
XX WPI; 2001-136877/14.
XX DR
XX In vitro cloning of nucleic acid involves mixing vectors comprising
XX recombination sites and/or nucleic acid, incubating mixture to produce
XX chimeric molecule, contacting hosts with mixture and selecting host.
XX PS
XX Claim 24; Col 46; 73pp; English.
XX CC
XX The present invention relates to a method for in vitro cloning of a
XX nucleic acid of interest. The method involves mixing in vitro two vectors
XX each comprising at least one recombination site and the nucleic acid of
XX interest; incubating the mixture in the presence of at least one
XX recombination protein to result in recombination of the recombination
XX sites, leading to production of a chimeric nucleic acid molecule
XX comprising the nucleic acid of interest; contacting hosts with the
XX mixture; and selecting for a host comprising the chimeric nucleic acid
XX molecule, and selecting against a host comprising the vectors comprising
XX the second vector, to clone the nucleic acid. The present sequence is a
XX recombination site, which may be used in the method of the present
XX invention
XX SQ
XX Sequence 25 BP; 4 A; 5 C; 3 G; 6 T; 0 U; 7 Other;

Query Match 84.8%; Score 21.2; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCGCTTTTKRTACNAACTSGB 25
Db 1 AGCCGCTTTTKRTACNAACTSGB 25

RESULT 5
AADI4430
ID AADI4430 standard; DNA; 25 BP.
XX
XX AADI4430;
XX AC
XX 01-NOV-2001 (first entry)
XX DT
XX Recombination site m-attB DNA.
XX DE
XX Recombination site; copy number; replicon; recombinatorial cloning;
XX m-attB; ds.
XX KW
XX Unidentified.
XX OS
XX US6270969-B1.
XX PN
XX 07-AUG-2001.
XX PD
XX

12-APR-2001 (first entry)
XX DT
XX DE
XX REcombination site m-attB.
XX KW
XX OS
XX Unidentified.
XX OS
XX US6171861-B1.
XX PN
XX 09-JAN-2001.
XX PD
XX 12-JAN-1998; 98US-00005476.
XX PF
XX 07-JUN-1995; 95US-00486139.
XX PR
XX 07-JUN-1996; 96US-00663002.
XX PA
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX PI
XX Hartley JL, Brasch MA;
XX WPI; 2001-136877/14.
XX DR
XX In vitro cloning of nucleic acid involves mixing vectors comprising
XX recombination sites and/or nucleic acid, incubating mixture to produce
XX chimeric molecule, contacting hosts with mixture and selecting host.
XX PS
XX Claim 24; Col 46; 73pp; English.
XX CC
XX The present invention relates to a method for in vitro cloning of a
XX nucleic acid of interest. The method involves mixing in vitro two vectors
XX each comprising at least one recombination site and the nucleic acid of
XX interest; incubating the mixture in the presence of at least one
XX recombination protein to result in recombination of the recombination
XX sites, leading to production of a chimeric nucleic acid molecule
XX comprising the nucleic acid of interest; contacting hosts with the
XX mixture; and selecting for a host comprising the chimeric nucleic acid
XX molecule, and selecting against a host comprising the vectors comprising
XX the second vector, to clone the nucleic acid. The present sequence is a
XX recombination site, which may be used in the method of the present
XX invention
XX SQ
XX Sequence 25 BP; 4 A; 5 C; 3 G; 6 T; 0 U; 7 Other;

Query Match 84.8%; Score 21.2; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCGCTTTTKRTACNAACTSGB 25
Db 1 AGCCGCTTTTKRTACNAACTSGB 25

RESULT 6
ABT16622
ID ABT16622 standard; DNA; 25 BP.
XX
XX ABT16622;
XX AC
XX 03-APR-2003 (first entry)
XX DT
XX Artificial plant chromosome related oligo SEQ ID No 34.
XX DE
XX Plant artificial chromosome; PAC; transgenic plant; vaccine;
XX blood factor; herbicide; stress; agronomical; nutrient quality;
XX bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
XX ds.
XX OS
XX Unidentified.
XX OS
XX WO200296923-A1.
XX PN
XX 05-DEC-2002.
XX PD
XX 30-MAY-2002; 2002WO-US017451.
XX PF
XX 30-MAY-2001; 2001US-0294687P.
XX PR
XX 04-JUN-2001; 2001US-0296329P.
XX PA
XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
XX (AGRI-) AGRISOMA INC.
XX
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PI Perez C, Fabijanski SF, Perkins E;
XX WPI; 2003-140436/13.
XX
XX Producing artificial chromosome by introducing a nucleic acid into plant
PT cell, selecting artificial chromosome that has one or more repeat regions
PT with equivalent amounts of euchromatic and heterochromatic nucleic acids.
XX
XX Disclosure; Page 261; 269pp; English.
XX
XX The invention relates to a novel method for producing plant artificial
CC chromosomes. The invention also relates to methods for targeting
CC insertion of heterologous DNA into plant artificial chromosomes, methods
CC for delivery of plant chromosomes to selected cells and tissues. The
CC isolated plant artificial chromosome (PAC) is useful for producing a
CC transgenic plant, which involves introducing the PAC into a plant cell.
CC The PAC comprises a heterologous nucleic acid encoding a gene product
CC such as enzymes, antisense RNA, rDNA, structural proteins, marker
CC proteins, ligands, receptors, ribozymes, therapeutic proteins, and
CC biopharmaceutical proteins, vaccines, blood factors, antigens, hormones,
CC cytokines, growth factors, antibodies, or a product that provides for
CC resistance to diseases, insects, herbicides, or stress in a plant. The
CC heterologous nucleic acid optionally encodes a product that provides an
CC agronomically important trait in the plant, e.g. a product that alters
CC nutrient use and/or improves the nutrient quality of the plant. The
CC heterologous nucleic acid is contained within a bacterial artificial
CC chromosome (BAC) or a yeast artificial chromosome (YAC). This
CC polynucleotide sequence represents an oligo relating to the method for
CC producing plant artificial chromosomes of the invention
XX
XX Sequence 25 BP; 4 A; 5 C; 3 G; 6 T; 0 U; 7 Other;
SQ
Query Match 84.8%; Score 21.2; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCCGCTTYYKTRTACNACTSG 25
Db 1 AGCCGCTTYYKTRTACNACTSG 25
RESULT 7
ACD28277
ID ACD28277 standard; DNA; 25 BP.
XX
XX ACD28277;
XX
XX 02-OCT-2003 (first entry)
XX
XX Nucleic acid core region m-attB.
XX
XX Core region; ds; vector donor DNA; flanking recombination site; m-attB.
XX
XX Synthetic.
XX
XX US2003064515-A1.
XX
XX 03-APR-2003.
XX
XX 30-JAN-2002; 2002US-00058291.
XX
XX 07-JUN-1995; 95US-00486139.
XX
XX 07-JUN-1996; 96US-00663002.
XX
XX 20-JAN-1999; 99US-00233493.
XX
XX 02-NOV-1999; 99US-00432085.
XX
XX (HART/) HARTLEY J L.
PA
XX (BRAS/) BRASCH M A.
XX
XX Hartley JL, Brasch MA;
XX
XX WPI; 2003-540791/51.
XX

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PT New Vector Donor DNA molecule for recombinational cloning using
PT engineered recombination sites, comprises first and second DNA segments
PT that do not recombine with each other and that contain a Selectable
PT marker.
XX
XX Claim 14; Page 25; 71pp; English.
XX
XX The invention relates to a vector donor DNA molecule comprising a first
CC DNA segment and a second DNA segment containing at least one selectable
CC marker. The first and second segments are separated either by, in a
CC circular vector donor, a first and a second recombination site, or in a
CC linear vector donor, at least a first recombination site, where each pair
CC of flanking recombination sites are engineered and do not recombine with
CC each other. The nucleic acid molecule, vectors and methods are useful for
CC moving or exchanging segments of DNA molecules using engineered
CC recombination sites and recombination proteins to provide chimeric DNA
CC molecules that have the desired characteristic(s) and/or DNA segment(s).
CC The present sequence represents the nucleic acid core region m-attB
XX
XX Sequence 25 BP; 4 A; 5 C; 3 G; 6 T; 0 U; 7 Other;
SQ
Query Match 84.8%; Score 21.2; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCCGCTTYYKTRTACNACTSG 25
Db 1 AGCCGCTTYYKTRTACNACTSG 25
RESULT 8
ACD28477
ID ACD28477 standard; DNA; 25 BP.
XX
XX ACD28477;
XX
XX 09-OCT-2003 (first entry)
XX
XX Nucleic acid core sequence m-attB.
XX
XX Nucleic acid core; m-attB; cointegrate DNA; flanking recombination site;
XX ds.
XX
XX Synthetic.
XX
XX US2003068799-A1.
XX
XX 10-APR-2003.
XX
XX 06-JUN-2002; 2002US-00162879.
XX
XX 07-JUN-1995; 95US-00486139.
XX
XX 07-JUN-1996; 96US-00663002.
XX
XX 20-JAN-1999; 99US-00233493.
XX
XX 02-NOV-1999; 99US-00432085.
XX
XX (INVI-) INVITROGEN CORP.
XX
XX Hartley JL, Brasch MA;
XX
XX WPI; 2003-540884/51.
XX
XX Making CoIntegrate DNA molecule, by combining recombination sites
PT flanking the desired DNA segment in insert donor DNA, with the
PT recombination sites of vector donor DNA, using site specific
PT recombination protein.
XX
XX Claim 14; Page 25; 71pp; English.
XX
XX The invention relates to a method of making a coIntegrate DNA molecule.
CC The method is useful for making a coIntegrate DNA molecule. The method is
CC useful for a variety of DNA exchanges, such as subcloning of DNA, in
CC vitro or in vivo. The method enables efficient and specific recombination
CC

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of DNA segments using recombination proteins. The method is highly specific, rapid and less labour intensive. The improved specificity, yield and speed of the method facilitates DNA or RNA subcloning, regulation and exchange useful for other related purposes. Since single molecules of the recombinations product can be introduced into a biological host, propagation of the desired product DNA in the absence of other DNA molecules is more readily realised. Reaction conditions can be freely adjusted in vitro to optimise enzyme activities. The present sequence represents the nucleic acid core sequence m-attB

SQ Sequence 25 BP; 4 A; 5 C; 3 G; 6 T; 0 U; 7 Other;

Query Match 84.8%; Score 21.2; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCGCTTYYKTRTACNAACTSG 25
Db 1 AGCCGCTTYYKTRTACNAACTSG 25

RESULT 9

ID ADA38163 standard; DNA; 25 BP.

XX ADA38163;

DT 20-NOV-2003 (first entry)

DE m-attB DNA sequence indicating generic core region of an attB site.

KW engineered recombination site; cloning; recombinase; subcloning; attB;
attP; attL; attR; selectable marker; cointegrate; m-attB; ds.

OS Synthetic.

PN US2003054552-A1.

PD 20-MAR-2003.

PF 30-JAN-2002; 2002US-00058292.

PR 07-JUN-1995; 95US-00486139.

PR 07-JUN-1996; 96US-00663002.

PR 20-JAN-1999; 99US-00233493.

PR 02-NOV-1999; 99US-00432085.

PA (HARTLEY) HARTLEY J L.

PA (BRAS) BRASCH M A.

PI Hartley JL, Brasch MA;

DR WPI; 2003-585168/55.

PT New Vector Donor DNA molecule, useful for recombinational cloning
purposes, comprises a first and a second DNA segment that contains a
selectable marker and is separated by a pair of flanking, engineered
recombination sites.

PS Claim 14; Page 26; 72pp; English.

This invention relates to novel DNA and vectors having engineered
recombination sites for use in a cloning method that enables efficient
and specific recombination of DNA segments using recombination proteins
including recombinases. As such, it provides a method for obtaining
chimeric nucleic acids with the desired characteristics, facilitating DNA
or RNA subcloning, regulation and/or exchange. The recombination site is
derived from attB, attP, attL or attR, where the att site is att1, att2 or
att3. Engineered mutations of the att sites (either one or multiple
mutations) can enhance specificity or efficiency of the recombination
reaction and the properties of the product DNA molecules. Accordingly,
the present invention describes a nucleic acid molecule comprising at
least one DNA segment having at least two engineered recombination sites

CC flanking a selectable marker and/or a desired DNA segment. Furthermore,
CC at least one of the engineered sites must enhance recombination in vitro
CC to form a cointegrate or product DNA molecule. This oligonucleotide
CC sequence is m-attB, a generic DNA sequence indicating the core region of
CC an attB recombination site of the invention.

XX Sequence 25 BP; 4 A; 5 C; 3 G; 6 T; 0 U; 7 Other;

Query Match 84.8%; Score 21.2; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCGCTTYYKTRTACNAACTSG 25
Db 1 AGCCGCTTYYKTRTACNAACTSG 25

RESULT 10

ID AAD60559 standard; DNA; 25 BP.

XX AAD60559;

DT 18-DEC-2003 (first entry)

DE Core region DNA, m-attB.

DE Recombinational cloning; DNA exchange; core region; ds.

OS Unidentified.

PN US2003100110-A1.

PD 29-MAY-2003.

PF 02-NOV-1999; 99US-00432085.

PR 07-JUN-1995; 95US-00486139.

PR 07-JUN-1996; 96US-00663002.

PR 20-JAN-1999; 99US-00233493.

PA (HARTLEY) HARTLEY J L.

PA (BRAS) BRASCH M A.

PI Hartley JL, Brasch MA;

DR WPI; 2003-730143/69.

PT New Vector Donor DNA molecule for recombinational cloning using
engineered recombination sites, comprises first and second DNA segments
that do not recombine with each other and that contain a selectable
marker.

PS Claim 14; Page 25; 71pp; English.

The invention relates to a vector donor DNA molecule which comprises
first and second DNA segments that do not recombine with each other and
that contain a selectable marker. The invention also relates to a method
for recombinational cloning using engineered recombination sites. The
invention is useful for moving or exchanging segments of DNA molecules
using engineered recombination sites and recombination proteins to
provide chimeric DNA molecules that have the desired characteristic(s)
and/or DNA segment(s). The present sequence is a core region DNA. This
sequence is used to illustrate the method of the invention

SQ Sequence 25 BP; 4 A; 5 C; 3 G; 6 T; 0 U; 7 Other;

Query Match 84.8%; Score 21.2; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCGCTTYYKTRTACNAACTSG 25
Db 1 AGCCGCTTYYKTRTACNAACTSG 25

```
Db      1  AGCCWGCCTTYYKTRTACNACTSGB 25

RESULT 11
ACC44651
ID  ACC44651 standard; DNA; 25 BP.
XX
AC  ACC44651;
XX
DT
XX
DE  29-MAY-2003 (first entry)
XX
DE  Recombination site related oligonucleotide SEQ ID NO:42.
XX
KW  Chromosome-based platform; artificial chromosome; eukaryotic chromosome;
KW  att site; integrase; recombinase; ACes; gene therapy; transgenic animal;
KW  platform artificial chromosome expression system; PCR primer; ss.
XX
OS  Synthetic.
XX
XX  WO200297059-A2.
XX
XX  05-DEC-2002.
XX
XX  30-MAY-2002; 2002WO-US017452.
XX
XX  30-MAY-2001; 2001US-0294758P.
XX
XX  21-MAR-2002; 2002US-0366891P.
XX
XX  (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
XX
XX  Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;
XX  Stewart S, Shellard J;
XX
XX  WPI; 2003-140461/13.
XX
XX  Novel eukaryotic chromosome comprising one or many att sites which
XX  permits site-directed integration in the presence of lambda-integrase,
XX  useful for site-specific recombination-directed integration of DNA of
XX  interest.
XX
XX  Claim 43; Page 143; 272pp; English.
XX
XX  The present invention describes a eukaryotic chromosome (I) comprising
XX  one or several att sites, where an att site is heterologous to the
XX  chromosome, and permits site-directed integration in the presence of
XX  lambda-integrase. Also described: (1) a platform artificial chromosome
XX  expression system (ACes) (II) comprising several sites that participate
XX  in recombinase catalysed recombination; and (2) a method (M1) for
XX  introducing a heterologous nucleic acid into a platform artificial
XX  chromosome. (I) can be used in gene therapy. (M1) is useful for
XX  introducing a heterologous nucleic acid molecule into a platform
XX  artificial chromosome, preferably an ACes. (II) is useful for producing a
XX  transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or
XX  mammal) by introducing (II) by cell fusion, lipid-mediated transfection
XX  by a carrier system, microinjection, microcell fusion, electroporation,
XX  microprojectile bombardment or direct DNA transfer into an embryonic
XX  cell, preferably a stem cell or an embryo. (II) comprises a heterologous
XX  nucleic acid that encodes a therapeutic product which is useful for
XX  making a library of ACes comprising random portions of a genome. ACC44612
XX  to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
XX  exemplification of the present invention
XX
XX  Sequence 25 BP; 4 A; 5 C; 3 G; 6 T; 0 U; 7 Other;
XX
Query Match      84.8%; Score 21.2; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. NO. 1.9; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1  AGCCWGCCTTYYKTRTACNACTSGB 25
|||||
Db      1  AGCCWGCCTTYYKTRTACNACTSGB 25
```

Qy 1 AGCCGCTTTTCTACNAACTSG 25
 Db 1 AGCCGCTTTTCTACNAACTSG 25

RESULT 13

AAX78974
 ID AAX78974 standard; DNA; 25 BP.

XX AAX78974;
 XX 17-AUG-1999 (first entry)
 XX Oligonucleotide #40 for recombination and cloning method.
 XX Cloning; donor; recombination site; vector; chimeric; ss.
 XX Synthetic.
 XX WO9921977-A1.

XX 06-MAY-1999.
 XX 26-OCT-1998; 98WO-US022589.
 XX 24-OCT-1997; 97US-0065930P.
 XX 23-OCT-1998; 98US-00177387.

XX (LIFE-) LIFE TECHNOLOGIES INC.
 XX Hartley JL, Brasch MA, Temple GF, Fox DK;
 XX WPI; 1999-303011/25.
 XX New nucleic acid cloning methods.

XX Disclosure; Page 170; 185pp; English.
 XX The invention relates to novel methods for cloning or subcloning one or more nucleic acid molecules (NMs) comprising: (a) combining in vitro or in vivo: (1) at least one insert donor molecules (IDMs) comprising one or more desired nucleic acid segments flanked by at least 2 recombination sites which do not recombine with each other; (2) one or more vector donor molecules (VDMs) comprising at least 2 recombination sites which do not recombine with each other; and (3) one or more site-specific recombination proteins; (b) incubating the combination to transfer one or more of the desired segments into one or more of the VDMs, thereby producing one or more desired product molecules (PMs). The methods can be used for the efficient and specific recombination of NAM segments. They can be used to generate chimeric DNA or RNA molecules that have the desired characteristics and/or nucleic acid segments. The methods can also be used for changing vectors. The oligonucleotides AAX78935-X78994 are used in the method of the invention

XX SQ Sequence 25 BP; 4 A; 4 C; 2 G; 7 T; 0 U; 8 Other;
 Query Match 81.6%; Score 20.4; DB 2; Length 25;
 Best Local Similarity 76.0%; Pred. No. 4.7;
 Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 AGCCGCTTTTCTACNAACTSG 25
 Db 1 ASCCGCTTTTCTACNAASTKG 25

RESULT 14

AAT48216
 ID AAT48216 standard; DNA; 25 BP.

XX AAT48216;
 XX 20-OCT-1997 (first entry)

XX attB2 core region.
 XX att recombination site; core region; mutation; enhance; recombination;
 XX vector; subcloning; regulation; exchange; ss.
 XX Synthetic.
 XX WO9640724-A1.
 XX 19-DEC-1996.
 XX 07-JUN-1996; 96WO-US010082.
 XX 07-JUN-1995; 95US-00486139.
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 XX Hartley JL, Brasch MA;
 XX WPI; 1997-065168/06.
 XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
 XX using recombinant proteins and engineered recombination sites in vitro or
 XX in vivo.
 XX Claim 14; Page 55; 106pp; English.
 XX AAT48210-25 are att recombination site core region DNA sequences. The
 XX core region has at least one engineered mutation that enhances
 XX recombination in vitro in the formation of a Cointegrate or Product DNA.
 XX These core regions can be incorporated into novel vector donor DNA
 XX molecules. The nucleic acids, vectors and methods of the invention are
 XX used to obtain chimeric nucleic acid using recombination proteins and
 XX engineered recombination sites in vitro or in vivo. The improved
 XX specificity, speed and yields of the invention facilitates DNA or RNA
 XX subcloning, regulation or exchange useful for any related purpose, e.g.
 XX in vitro recombination of DNA segments, and in vitro or in vivo insertion
 XX or modification of transcribed, replicated, isolated or genomic DNA or
 XX RNA
 XX SQ Sequence 25 BP; 5 A; 6 C; 4 G; 10 T; 0 U; 0 Other;
 Query Match 80.0%; Score 20; DB 2; Length 25;
 Best Local Similarity 72.0%; Pred. No. 7.4;
 Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 AGCCGCTTTTCTACNAACTSG 25
 Db 1 AGCCTGCTTTCTGTACAACTTGT 25
 RESULT 15
 AAT48215
 ID AAT48215 standard; DNA; 25 BP.
 XX AAT48215;
 XX 20-OCT-1997 (first entry)
 XX attB1 core region.
 XX att recombination site; core region; mutation; enhance; recombination;
 XX vector; subcloning; regulation; exchange; ss.
 XX Synthetic.
 XX WO9640724-A1.
 XX 19-DEC-1996.
 XX 07-JUN-1996; 96WO-US010082.
 XX

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PR 07-JUN-1995; 95US-004861139.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Hartley JL, Braesch MA;
XX
XX WPI; 1997-065168/06.
XX
XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
PT using recombinant proteins and engineered recombination sites in vitro or
PT in vivo.
XX
XX Claim 14; Page 55; 106pp; English.
XX
XX AAT48210-25 are att recombination site core region DNA sequences. The
CC core region has at least one engineered mutation that enhances
CC recombination in vitro in the formation of a Cointegrate or Product DNA.
CC These core regions can be incorporated into novel vector donor DNA
CC molecules. The nucleic acids, vectors and methods of the invention are
CC used to obtain chimeric nucleic acid using recombination proteins and
CC engineered recombination sites in vitro or in vivo. The improved
CC specificity, speed and yields of the invention facilitates DNA or RNA
CC subcloning, regulation or exchange useful for any related purpose, e.g.
CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
CC or modification of transcribed, replicated, isolated or genomic DNA or
XX RNA
XX
XX Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 U; 0 Other;
XX
XX Query Match 80.0%; Score 20; DB 2; Length 25;
XX Best Local Similarity 72.0%; Pred. No. 7.4;
XX Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0
XX
QY 1 AGCCWGCCTTYYKTRTACNAACTSGB 25
XX |||||:|||||:|||||:
Db 1 AGCGCTGCTTTTGTACAAACTGT 25
XX
Search completed: November 16, 2004, 04:02:45
Job time : 168.8 secs

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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:19 ; Search time 35.9 Seconds
(without alignments)
494.978 Million cell updates/sec

Title: US-10-820-133-2

Perfect score: 25
Sequence: 1 agcwgcttyktrtaacnaactsgb 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	21.2	84.8	25	3	US-09-005-476-2
3	21.2	84.8	25	3	US-09-233-492-2
4	21.2	84.8	25	3	US-09-296-280-2
5	21.2	84.8	25	4	US-09-498-074-2
6	21.2	84.8	25	4	US-09-498-074-2
7	21.2	84.8	25	5	PCT-US96-10082A-2
8	20.4	81.6	25	3	US-09-296-280-40
9	20	80.0	25	3	US-09-233-493-6
10	20	80.0	25	3	US-09-233-493-7
11	20	80.0	25	3	US-09-233-493-33
12	20	80.0	25	3	US-09-233-493-34
13	20	80.0	25	3	US-09-005-476-6
14	20	80.0	25	3	US-09-005-476-7
15	20	80.0	25	3	US-09-005-476-33
16	20	80.0	25	3	US-09-005-476-34
17	20	80.0	25	3	US-09-233-492-6
18	20	80.0	25	3	US-09-233-492-7
19	20	80.0	25	3	US-09-233-492-33
20	20	80.0	25	3	US-09-233-492-34
21	20	80.0	25	3	US-09-296-280-6
22	20	80.0	25	3	US-09-296-280-7
23	20	80.0	25	4	US-09-498-074-6
24	20	80.0	25	4	US-09-498-074-7
25	20	80.0	25	4	US-09-498-074-33
26	20	80.0	25	4	US-09-498-074-34
27	20	80.0	25	4	US-09-498-074-6

Sequence 7, Appli
Sequence 33, Appli
Sequence 34, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 56, Appli
Sequence 15, Appli
Sequence 50, Appli
Sequence 63, Appli
Sequence 12, Appli
Sequence 58, Appli
Sequence 52, Appli
Sequence 359, App
Sequence 739, App
Sequence 587, App
Sequence 3, Appli

28 20 80.0 25 4 US-09-498-074-7
c 29 20 80.0 25 4 US-09-498-074-33
c 30 20 80.0 25 4 US-09-498-074-34
31 20 80.0 25 5 PCT-US96-10082A-6
32 20 80.0 25 5 PCT-US96-10082A-7
c 33 20 80.0 48 3 US-09-296-280-56
c 34 20 80.0 48 4 US-09-944-807-15
c 35 20 80.0 49 3 US-09-296-280-50
c 36 20 80.0 49 4 US-09-935-916B-63
c 37 20 80.0 50 4 US-10-004-993A-12
c 38 20 80.0 52 3 US-09-296-280-58
c 39 20 80.0 53 3 US-09-296-280-52
c 40 20 80.0 656 4 US-09-774-528-359
c 41 20 80.0 970 4 US-09-636-215-739
c 42 20 80.0 970 4 US-09-685-166A-739
c 43 20 80.0 970 4 US-09-679-426-739
c 44 20 80.0 1244 4 US-09-799-451-587
c 45 20 80.0 1357 4 US-09-668-680-3

ALIGNMENTS

RESULT 1
US-09-233-493-2
; Sequence 2, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Braach, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
US-09-233-493-2

Query Match 84.8%; Score 21.2; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCGCTTTTKRTACNAACTSGB 25
|||||
Db 1 AGCCGCTTTTKRTACNAACTSGB 25

RESULT 2

US-09-005-476-2
; Sequence 2, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-2

Query Match 84.8%; Score 21.2; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGCCGCTTTTKRTACNAACTSGB 25
|||||
Db 1 AGCCGCTTTTKRTACNAACTSGB 25

RESULT 3

US-09-233-492-2
; Sequence 2, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington

; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-492-2

Query Match 84.8%; Score 21.2; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGCCGCTTTTKRTACNAACTSGB 25
|||||
Db 1 AGCCGCTTTTKRTACNAACTSGB 25

RESULT 4

US-09-296-280-2
; Sequence 2, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-2


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Query Match      84.8%; Score 21.2; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTYYKTRTACNAACTSGB 25
    |||||
Db 1 AGCCWGCCTTYYKTRTACNAACTSGB 25

RESULT 5
US-09-498-074-2
; Sequence 2, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-498-074-2

Query Match      84.8%; Score 21.2; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTYYKTRTACNAACTSGB 25
    |||||
Db 1 AGCCWGCCTTYYKTRTACNAACTSGB 25

RESULT 6
US-09-498-074-2
; Sequence 2, Application US/09498074
; Patent No. 6720140
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-498-074-2

Query Match      84.8%; Score 21.2; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTYYKTRTACNAACTSGB 25
    |||||
Db 1 AGCCWGCCTTYYKTRTACNAACTSGB 25

RESULT 7
PCT-US96-10082A-2
; Sequence 2, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-498-074-2
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APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
RECOMBINATION SITES
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,074
FILING DATE: 04-Feb-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-498-074-2

Query Match      84.8%; Score 21.2; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTYYKTRTACNAACTSGB 25
    |||||
Db 1 AGCCWGCCTTYYKTRTACNAACTSGB 25

RESULT 7
PCT-US96-10082A-2
; Sequence 2, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: 04-Feb-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-498-074-2
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/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US96/10082A
/ FILING DATE: 07-JUN-1996
/ CLASSIFICATION:
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: both
/ MOLECULE TYPE: cdna
PCT-US96-10082A-2

Query Match      84.8%; Score 21.2; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCGCTTTTXYKTRTACNAACTSGB 25
Db 1 AGCCGCTTTTXYKTRTACNAACTSGB 25

RESULT 8
US-09-296-280-40
/ Sequence 40, Application US/09296280
/ Patent No. 6277608
/ GENERAL INFORMATION:
/ APPLICANT: Hartley, James L.
/ APPLICANT: Brasch, Michael A.
/ APPLICANT: Temple, Gary F.
/ APPLICANT: Fox, Donna K.
/ TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
/ TITLE OF INVENTION: Recombination Sites
/ FILE REFERENCE: 0942.285007
/ CURRENT APPLICATION NUMBER: US/09/296,280
/ EARLIER FILING DATE: 1999-04-22
/ EARLIER APPLICATION NUMBER: US 09/177,387
/ EARLIER FILING DATE: 1998-10-23
/ EARLIER APPLICATION NUMBER: US 60/065,930
/ EARLIER FILING DATE: 1997-10-24
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 40
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Description of Unknown Organism: recombination
US-09-296-280-40

Query Match      81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.37;
Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCCGCTTTTXYKTRTACNAACTSGB 25
Db 1 ASCCGCTTTTXYKTRTACNAACTSGB 25

RESULT 9
US-09-233-493-6
/ Sequence 6, Application US/09233493
/ Patent No. 6143557
/ GENERAL INFORMATION:
/ APPLICANT: Hartley, James L.
/ APPLICANT: Brasch, Michael A.
/ TITLE OF INVENTION: Recombinational Cloning Using Engineered
/ TITLE OF INVENTION: Recombination Sites
```

```
/ NUMBER OF SEQUENCES: 35
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
/ STREET: 1100 New York Ave., N. W. Suite 600
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3934
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/233,493
/ FILING DATE: 20-JAN-1999
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/005,476
/ FILING DATE: 12-JAN-1998
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/663,002
/ FILING DATE: 07-JUN-1996
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/486,139
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION:
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: both
/ MOLECULE TYPE: cdna
US-09-233-493-6

Query Match      80.0%; Score 20; DB 3; Length 25;
Best Local Similarity 72.0%; Pred. No. 0.59;
Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGCCGCTTTTXYKTRTACNAACTSGB 25
Db 1 AGCCTGCTTTTGTACAACTTGT 25

RESULT 10
US-09-233-493-7
/ Sequence 7, Application US/09233493
/ Patent No. 6143557
/ GENERAL INFORMATION:
/ APPLICANT: Hartley, James L.
/ APPLICANT: Brasch, Michael A.
/ TITLE OF INVENTION: Recombinational Cloning Using Engineered
/ TITLE OF INVENTION: Recombination Sites
/ NUMBER OF SEQUENCES: 35
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
/ STREET: 1100 New York Ave., N. W. Suite 600
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3934
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-493-7

Query Match 80.0%; Score 20; DB 3; Length 25;
Best Local Similarity 72.0%; Pred. No. 0.59;
Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCCGCTTYYKTRTACNAACTSGB 25
|||||:|||||:|||||:
Db 1 AGCCTGCTTCTGTACAACTGT 25

RESULT 11
US-09-233-493-33/c
Sequence 33, Application US/09233493
Patent No. 6143557
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995

CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-493-33

Query Match 80.0%; Score 20; DB 3; Length 25;
Best Local Similarity 72.0%; Pred. No. 0.59;
Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCCGCTTYYKTRTACNAACTSGB 25
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Db 25 AGCCTGCTTCTGTACAACTGT 1

RESULT 12
US-09-233-493-34/c
Sequence 34, Application US/09233493
Patent No. 6143557
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-493-34

Query Match 80.0%; Score 20; DB 3; Length 25;

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Best Local Similarity 72.0%; Pred. No. 0.59;
Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTYYKTRTACNAACTSGB 25
Db 25 AGCCYGCCTTCTGTACAACTTGT 1

RESULT 13
US-09-005-476-6
; Sequence 6, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-005-476-7

Query Match 80.0%; Score 20; DB 3; Length 25;
Best Local Similarity 72.0%; Pred. No. 0.59;
Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTYYKTRTACNAACTSGB 25
Db 1 AGCCTGCTTCTGTACAACTTGT 25

RESULT 15
US-09-005-476-33/c
; Sequence 33, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-005-476-6

Query Match 80.0%; Score 20; DB 3; Length 25;
Best Local Similarity 72.0%; Pred. No. 0.59;
Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTYYKTRTACNAACTSGB 25
Db 1 AGCCTGCTTCTGTACAACTTGT 25

RESULT 14
US-09-005-476-7
; Sequence 7, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
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; MOLECULE TYPE: cDNA
US-09-005-476-33

Query Match 80.0%; Score 20; DB 3; Length 25;
Best Local Similarity 72.0%; Pred. No. 0.59;
Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCCGCTTTTYYKRTACNAACTSG 25
|||:|||||:|||||:
Db 25 AGCCTGCTTTTGTACAACTTGT 1

Search completed: November 16, 2004, 10:22:30
Job time : 36.9 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:34:49 ; Search time 314 Seconds
(without alignments)
430.015 Million cell updates/sec

Title: US-10-820-133-2

Perfect score: 25

Sequence: 1 agcwgcttcttactnaactsgb 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21.2	84.8	25	9	US-09-855-797A-2
2	21.2	84.8	25	9	US-09-907-900-2
3	21.2	84.8	25	9	US-09-907-719-2
4	21.2	84.8	25	10	US-09-432-085-2
5	21.2	84.8	25	10	US-09-985-448-2
6	21.2	84.8	25	14	US-10-058-292-2
7	21.2	84.8	25	14	US-10-058-291-2
8	21.2	84.8	25	14	US-10-162-879-2
9	21.2	84.8	25	15	US-10-161-403-2
10	21.2	84.8	25	15	US-10-300-892-2
11	21.2	84.8	25	16	US-10-680-316-2
12	21.2	84.8	25	17	US-10-815-730-2

13	21.2	84.8	25	17	US-10-820-133-2	Sequence 2, Appli
14	21.2	84.8	25	18	US-10-161-408-34	Sequence 34, Appli
15	21.2	84.8	25	18	US-10-796-868A-2	Sequence 2, Appli
16	20.4	81.6	25	9	US-09-855-797A-40	Sequence 40, Appli
17	20.4	81.6	25	9	US-09-907-900-40	Sequence 40, Appli
18	20.4	81.6	25	9	US-09-907-719-40	Sequence 40, Appli
19	20.4	81.6	25	10	US-09-985-448-40	Sequence 40, Appli
20	20.4	81.6	25	15	US-10-300-892-40	Sequence 40, Appli
21	20.4	81.6	25	16	US-10-680-316-40	Sequence 40, Appli
22	20.4	81.6	25	17	US-10-815-730-40	Sequence 40, Appli
23	20.4	81.6	25	17	US-10-820-133-40	Sequence 40, Appli
24	20	80.0	25	9	US-09-732-914-5	Sequence 5, Appli
25	20	80.0	25	9	US-09-855-797A-6	Sequence 6, Appli
26	20	80.0	25	9	US-09-855-797A-7	Sequence 7, Appli
27	20	80.0	25	9	US-09-907-900-6	Sequence 6, Appli
28	20	80.0	25	9	US-09-907-900-7	Sequence 7, Appli
29	20	80.0	25	9	US-09-907-719-6	Sequence 6, Appli
30	20	80.0	25	9	US-09-907-719-7	Sequence 7, Appli
31	20	80.0	25	10	US-09-432-085-6	Sequence 6, Appli
32	20	80.0	25	10	US-09-432-085-7	Sequence 7, Appli
33	20	80.0	25	10	US-09-432-085-33	Sequence 33, Appli
34	20	80.0	25	10	US-09-432-085-34	Sequence 34, Appli
35	20	80.0	25	10	US-09-985-448-6	Sequence 6, Appli
36	20	80.0	25	10	US-09-985-448-7	Sequence 7, Appli
37	20	80.0	25	14	US-10-168-774-1	Sequence 1, Appli
38	20	80.0	25	14	US-10-055-001A-1	Sequence 1, Appli
39	20	80.0	25	14	US-10-055-001A-2	Sequence 2, Appli
40	20	80.0	25	14	US-10-058-292-6	Sequence 6, Appli
41	20	80.0	25	14	US-10-058-292-7	Sequence 7, Appli
42	20	80.0	25	14	US-10-058-292-33	Sequence 33, Appli
43	20	80.0	25	14	US-10-058-292-34	Sequence 34, Appli
44	20	80.0	25	14	US-10-058-291-6	Sequence 6, Appli
45	20	80.0	25	14	US-10-058-291-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1

US-09-855-797A-2
Sequence 2, Application US/09855797A
Patent No. US20020094574A1
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Fox, Donna K.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.285008
CURRENT APPLICATION NUMBER: US/09/855.797A
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/296,281
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: US 60/065,930
PRIOR FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 25
TYPE: DNA
ORGANISM: Unknown
FEATURE:
NAME/KEY: OTHER
LOCATION: 18
OTHER INFORMATION: "n" may be any nucleotide
OTHER INFORMATION: Description of Unknown Organism: recombination
OTHER INFORMATION: products
US-09-855-797A-2

Query Match 84.8%; Score 21.2; DB 9; Length 25;

Best Local Similarity 100.0%; Pred. No. 1.5;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
US-09-985-448-2
; Sequence 2, Application US/09985448
; Publication No. US20030157716A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/985,448
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-985-448-2

Query Match 84.8%; Score 21.2; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCGCTTTTKRTACNAACTSGB 25
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Db 1 AGCCGCTTTTKRTACNAACTSGB 25

RESULT 6
US-10-058-292-2
; Sequence 2, Application US/10058292
; Publication No. US20030054552A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/058,292
; FILING DATE: 30-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/432,085
; FILING DATE: 1999-11-02
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 1999-11-02
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999

; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-058-292-2

Query Match 84.8%; Score 21.2; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCGCTTTTKRTACNAACTSGB 25
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Db 1 AGCCGCTTTTKRTACNAACTSGB 25

RESULT 7
US-10-058-291-2
; Sequence 2, Application US/10058291
; Publication No. US20030064515A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/058,291
; FILING DATE: 30-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/432,085
; FILING DATE: 1999-11-02
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both

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;
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-058-291-2

Query Match      84.8%; Score 21.2; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTYYKTRTACNAACTSG 25
Db 1 AGCCWGCCTTYYKTRTACNAACTSG 25

RESULT 8
US-10-162-879-2
; Sequence 2, Application US/10162879
; Publication No. US20030068799A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/162,879
; FILING DATE: 06-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-162-879-2

Query Match      84.8%; Score 21.2; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTYYKTRTACNAACTSG 25
Db 1 AGCCWGCCTTYYKTRTACNAACTSG 25
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RESULT 9
US-10-161-403-42
; Sequence 42, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: m-attB;
; FEATURE:
; NAME/KEY: misc_difference
; LOCATION: 18
; OTHER INFORMATION: n is a o r g o r c o r t/u
US-10-161-403-42

Query Match      84.8%; Score 21.2; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTYYKTRTACNAACTSG 25
Db 1 AGCCWGCCTTYYKTRTACNAACTSG 25

RESULT 10
US-10-300-892-2
; Sequence 2, Application US/10300892
; Publication No. US20030175970A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/300,892
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; FEATURE:
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;; APPLICANT: Perkins, Edward
;; TITLE OF INVENTION: Plant Artificial Chromosomes, Uses thereof, and Methods of Preparation
;; FILE REFERENCE: 24601-419
;; CURRENT APPLICATION NUMBER: US/10/161,408
;; CURRENT FILING DATE: 2002-05-30
;; PRIOR APPLICATION NUMBER: US 60/294,687
;; PRIOR FILING DATE: 2001-05-30
;; PRIOR APPLICATION NUMBER: US 60/296,329
;; PRIOR FILING DATE: 2001-06-04
;; NUMBER OF SEQ ID NOS: 51
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 34
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: m-attB recognition sequence
;; NAME/KEY: misc_difference
;; LOCATION: 18
;; OTHER INFORMATION: n is a or c or g or t/u
US-10-161-408-34

Query Match 84.8%; Score 21.2; DB 18; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTYKTRTACNAACTSGB 25
|||
Db 1 AGCCWGCCTTYKTRTACNAACTSGB 25

RESULT 15

US-10-796-868A-2
;; Sequence 2, Application US/10796868A
;; Publication No. US20040219673A1
;; GENERAL INFORMATION:
;; APPLICANT: Braesch, Michael A.
;; TITLE OF INVENTION: Recombinational Cloning Using Engineered Recombination Sites
;; FILE REFERENCE: 0942.285000K
;; CURRENT APPLICATION NUMBER: US/10/796,868A
;; CURRENT FILING DATE: 2004-03-10
;; PRIOR APPLICATION NUMBER: US 09/498,074
;; PRIOR FILING DATE: 2000-02-04
;; PRIOR APPLICATION NUMBER: US 09/005,476
;; PRIOR FILING DATE: 1998-01-12
;; PRIOR APPLICATION NUMBER: US 08/663,002
;; PRIOR FILING DATE: 1996-06-07
;; PRIOR APPLICATION NUMBER: US 08/486,139
;; PRIOR FILING DATE: 1995-06-07
;; NUMBER OF SEQ ID NOS: 35
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 2
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Unknown
;; FEATURE:
;; OTHER INFORMATION: m-attB core region
;; NAME/KEY: misc feature
;; LOCATION: (18)..(18)
;; OTHER INFORMATION: n is a, c, g, or t/u
US-10-796-868A-2

Query Match 84.8%; Score 21.2; DB 18; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTYKTRTACNAACTSGB 25
|||
Db 1 AGCCWGCCTTYKTRTACNAACTSGB 25

Search completed: November 16, 2004, 11:14:58
Job time : 315.1 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:04 ; Search time 1532 Seconds
(without alignments)
594.643 Million cell updates/sec

Title: US-10-820-133-2

Perfect score: 25

Sequence: 1 agccwgcttcttactaactagb 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:

1: gb_est1:*
2: gb_est2:*
3: gb_hcc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21.2	84.8	888	7	CK209237 FGAS02099
2	21.2	84.8	1012	7	CK211630 FGAS02348
3	21.2	84.8	1031	7	CK163965 FGAS01660
4	21.2	84.8	1031	7	CK212789 FGAS02467
5	21.2	84.8	1043	7	CK212830 FGAS02472
6	21.2	84.8	1051	7	CK212815 FGAS02470
7	21.2	84.8	1053	7	CK212320 FGAS02419
8	21.2	84.8	1059	7	CK163940 FGAS01658
9	21.2	84.8	1062	7	CK212429 FGAS02430
10	21.2	84.8	1067	7	CK212431 FGAS02430
11	21.2	84.8	1070	7	CK2113073 FGAS02497
12	21.2	84.8	1071	7	CK211886 FGAS02374
13	21.2	84.8	1071	7	CK212465 FGAS02433
14	21.2	84.8	1076	7	CK216054 FGAS02803
15	21.2	84.8	1082	7	CK212170 FGAS02403
16	21.2	84.8	1088	7	CK205724 FGAS01725
17	21.2	84.8	1093	7	CK211774 FGAS02362
18	21.2	84.8	1095	7	CK212335 FGAS02420
19	21.2	84.8	1098	7	CK213245 FGAS02515
20	21.2	84.8	1102	7	CK214856 FGAS02679
21	21.2	84.8	1113	7	CK207537 FGAS01916
22	21.2	84.8	1113	7	CK216493 FGAS02848
23	21.2	84.8	1119	7	CK214588 FGAS02651
24	21.2	84.8	1124	7	CK211806 FGAS02366

25	21.2	84.8	1147	7	CK211595
26	21.2	84.8	1156	7	CK205566
27	21.2	84.8	1175	7	CK211649
28	20	80.0	83	6	CB398074
C 29	20	80.0	83	6	CB401650
C 30	20	80.0	109	6	CB103959
C 31	20	80.0	141	6	CB103917
C 32	20	80.0	190	4	BI477091
C 33	20	80.0	201	4	BG775739
C 34	20	80.0	214	5	EX347917
C 35	20	80.0	221	6	CB104038
C 36	20	80.0	223	5	EX347916
C 37	20	80.0	275	7	CK447077
C 38	20	80.0	281	2	BE612945
C 39	20	80.0	307	7	CF857529
40	20	80.0	336	5	BP776084
41	20	80.0	337	2	BE672796
42	20	80.0	347	4	BI446328
C 43	20	80.0	358	6	CB103951
C 44	20	80.0	363	6	CB103941
45	20	80.0	367	5	BP776789

ALIGNMENTS

RESULT 1
CK209237
LOCUS
DEFINITION FGAS020994 Triticum aestivum FGAS: Library 5 GATE 7 Triticum
aestivum CDNA, mRNA sequence.
CK209237
CK209237.1 GI:39571627
EST.
Triticum aestivum (bread wheat)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 888)

REFERENCE
AUTHORS
Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,
Genevieve, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,
Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,
Penniket, C., Roach, J.L., and Sarhan, F.
Functional Genomics of Abiotic Stress in Wheat and Canola Crops
Unpublished (2003)
Contact: Wm L Crosby
Bioinformatics
University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas_esta@cs.usask.ca
This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [11,663].
Plate: L5B016 row: N column: 13.
Location/Qualifiers
1. .888
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone_lib="Triticum aestivum FGAS: Library 5 GATE 7"
/note="Vector: pCMV.SP0R16; Crown and developmental stages
of spike formation in wheat cultivar Norstar. 4 mRNA
populations were combined before constructing the library.
The first mRNA population is from 1cm crown sections after
30 days of cold acclimation. The second is from 1cm crown
sections after 11 days of deacclimation (before
deacclimation plants were fully vernalized for 49 days).

FEATURES

source
Location/Qualifiers
1. .888
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone_lib="Triticum aestivum FGAS: Library 5 GATE 7"
/note="Vector: pCMV.SP0R16; Crown and developmental stages
of spike formation in wheat cultivar Norstar. 4 mRNA
populations were combined before constructing the library.
The first mRNA population is from 1cm crown sections after
30 days of cold acclimation. The second is from 1cm crown
sections after 11 days of deacclimation (before
deacclimation plants were fully vernalized for 49 days).

temperature exposure. The last 6 populations: After 7 days of growth at 20C, wheat plants were transferred to 4C in the dark. 1cm crown sections and green leaf tissue were separately harvested after 1, 3, and 6 hours of low temperature exposure. First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with NotI. In addition, this library used a primer for second strand synthesis that annealed to an artificial sequence (RNA oligo) added before first strand synthesis. Therefore when sequences from EST generated from this library will be masked for vector and adaptor sequences, an additional masking step will have to be included to mask this RNA oligo that is common to all clones (sequence CGACTGGAGCAGGACACTGACATGCTGAGGAGTAGAAA)."

ORIGIN

Query Match 84.8%; Score 21.2; DB 7; Length 1043;
Best Local Similarity 72.0%; Pred. No. 24;
Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTYYKTRTACNAACTSGB 25

Db 927 AGCCTGCTTTTGTACAACTGGT 951

RESULT 6
CK212815
LOCUS CK212815 1051 bp mRNA linear EST 09-DEC-2003
DEFINITION FGAS024704 Triticum aestivum FGAS: Library 6 CAP GATE 1 Triticum
aestivum cDNA, mRNA sequence.

ACCESSION CK212815

VERSION CK212815.1 GI:39618919

KEYWORDS EST.

SOURCE Triticum aestivum (bread wheat)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.

1 (bases 1 to 1051)

Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,
Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,
Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,
Penniket, C., Roach, J.L. and Sarhan, F.

Functional Genomics of Abiotic Stress In Wheat and Canola Crops

Unpublished (2003)

Contact: Wm L Crosby

Bioinformatics

University of Saskatchewan, Department of Computer Science

1C101 Engineering Building, 57 Campus Drive, Saskatoon,

Saskatchewan, S7N 5A9, Canada

Tel: 306 966 1769

Fax: 306 966 2033

Email: fgas_est@cs.usask.ca

This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified

the region [55,784].

Plate: L6B007 row: B column: 19.

Location/Qualifiers

1..1051

/organism="Triticum aestivum"

/mol_type="mRNA"

/db_xref="taxon:4565"

/clone_lib="Triticum aestivum FGAS: Library 6 CAP GATE 1"
/note="Organ: Crown and leaf; Vector: PCMV.SPORT6; Crown
(50%) and leaf (50%) tissues from wheat cultivar Norstar
after short exposure times to low temperature in the light
and in the dark. 12 mRNA populations were combined before
constructing the library. The first 6 populations: After 7
days of growth at 20Cs from wheat cultivar Norstar after
short exposure times to low temperature in the light and

in the dark. 12 mRNA populations were combined before
constructing the library. The first 6 populations: After 7
days of growth at 20, wheat plants were transferred to 4C
in the light. 1cm crown sections and green leaf tissue were
separately harvested after 1, 3, and 6 hours of low
temperature exposure. The last 6 populations: After 7 days
of growth at 20C, wheat plants were transferred to 4C in
the dark. 1cm crown sections and green leaf tissue were
separately harvested after 1, 3, and 6 hours of low
temperature exposure. First strand synthesis in this
library was done in the presence of methylated dCTP
thereby protecting from internal cleavage with NotI. In
addition, this library used a primer for second strand
synthesis that annealed to an artificial sequence (RNA
oligo) added before first strand synthesis. Therefore when
sequences from EST generated from this library will be
masked for vector and adaptor sequences, an additional
masking step will have to be included to mask this RNA
oligo that is common to all clones (sequence
CGACTGGAGCAGGACACTGACATGCTGAGGAGTAGAAA)."

ORIGIN

Query Match 84.8%; Score 21.2; DB 7; Length 1051;
Best Local Similarity 72.0%; Pred. No. 24;
Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTYYKTRTACNAACTSGB 25

Db 843 AGCCTGCTTTTGTACAACTGGT 867

RESULT 7

CK212320

LOCUS CK212320 1053 bp mRNA linear EST 09-DEC-2003

DEFINITION FGAS024191 Triticum aestivum FGAS: Library 6 CAP GATE 1 Triticum

aestivum cDNA, mRNA sequence.

ACCESSION CK212320

VERSION CK212320.1 GI:39618424

KEYWORDS EST.

SOURCE Triticum aestivum (bread wheat)

ORGANISM

Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticeae; Triticum.

1 (bases 1 to 1053)

Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,

Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,

Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,

Penniket, C., Roach, J.L. and Sarhan, F.

Functional Genomics of Abiotic Stress In Wheat and Canola Crops

Unpublished (2003)

Contact: Wm L Crosby

Bioinformatics

University of Saskatchewan, Department of Computer Science

1C101 Engineering Building, 57 Campus Drive, Saskatoon,

Saskatchewan, S7N 5A9, Canada

Tel: 306 966 1769

Fax: 306 966 2033

Email: fgas_est@cs.usask.ca

This sequence is the direct result of the Base calling software

Phred (default parameters). It is the raw base calls. To aid in the

identification of the high quality insert the software Lucy

(default parameters) has been run on this sequence. Lucy identified

the region [22,725].

Plate: L6B005 row: E column: 09.

Location/Qualifiers

1..1053

/organism="Triticum aestivum"

/mol_type="mRNA"

/db_xref="taxon:4565"

/clone_lib="Triticum aestivum FGAS: Library 6 CAP GATE 1"

/note="Organ: Crown and leaf; Vector: PCMV.SPORT6; Crown

(50%) and leaf (50%) tissues from wheat cultivar Norstar

after short exposure times to low temperature in the light

and in the dark. 12 mRNA populations were combined before

constructing the library. The first 6 populations: After 7

days of growth at 20Cs from wheat cultivar Norstar after

short exposure times to low temperature in the light and

after short exposure times to low temperature in the light and in the dark. 12 mRNA populations were combined before constructing the library. The first 6 populations: After 7 days of growth at 20°Cs from wheat cultivar Norstar after short exposure times to low temperature in the light and in the dark. 12 mRNA populations were combined before constructing the library. The first 6 populations: After 7 days of growth at 20, wheat plants were transferred to 4°C in the light. 1cm crown sections and green leaf tissue were separately harvested after 1, 3, and 6 hours of low temperature exposure. The last 6 populations: After 7 days of growth at 20°C, wheat plants were transferred to 4°C in the dark. 1cm crown sections and green leaf tissue were separately harvested after 1, 3, and 6 hours of low temperature exposure. First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with NotI. In addition, this library used a primer for second strand synthesis that annealed to an artificial sequence (RNA oligo) added before first strand synthesis. Therefore when sequences from EST generated from this library will be masked for vector and adaptor sequences, an additional masking step will have to be included to mask this RNA oligo that is common to all clones (sequence: CGACTCGACACGACGACTGACATGCATGCAGGAGGTAGAAA). "

ORIGIN

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Query Match      84.8%; Score 21.2; DB 7; Length 1053;
Best Local Similarity 72.0%; Pred. No. 24;
Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
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QY 1 AGCCGCGCTTYYKTRTACNAACTSGB 25
|||||:|||||:|||||:|||||:|
Db 819 AGCCTGCTTTTGTACAAACTGGT 843

RESULT 8					
CK163940					
LOCUS					
DEFINITION	CK163940	1059 bp	mRNA	linear	EST 05-DEC-2003
	FGAS016580				
	Triticum aestivum FGAS: Library 4 Gate 8 Triticum				
	aestivum cDNA, mRNA sequence.				

ACQUARDUS	SOURCE	ORGANISM
251.		
	Triticum aestivum (bread wheat)	
	Triticum aestivum	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	
	Poideae; Triticeae; Triticum.	

TITLE Functional Genomics of Abiotic Stress In Wheat and Canola Crops
JOURNAL Unpublished (2003)
COMMENT Contact: Wm L Crosby

Rax: 306 966 2033
Email: fgas_estacs.usask.ca

This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [85,522].

FEATURES
SOURCE

/mol_type="mRNA"
/db_xref="taxon:4565"
/clone_lib="Trilicum aestivum FGAS: Library 4 Gate 8"
/Notes="Organ: Crown and leaf; Vector: pCMV.SPORTS;
Conditions: Growth and leaf: Seeds were germinated in a
water-saturated mix (50% black earth and 50% ProMix) in a
growth chamber for 7 days under an irradiance of 200 mmol
m⁻² sec⁻¹. The temperature was maintained at 20 degrees C
with a 15-hr photoperiod under a relative humidity of 70%.
After this period watering of plants was stopped. Four
time points were sampled during a two week period; the
first after wilting was observed and the last, two weeks
later, consisted of live crown and leaf tissue (leaf
tissue that was yellow was not included in sampled
material). First strand synthesis in this library was done
in the presence of methylated dCTP thereby protecting from
internal cleavage with NotI."

ORIGIN

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Query Match      84.8%; Score 21.2; DB 7; Length 1059;
Best Local Similarity 72.0%; Pred. No. 24;
Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 AGCCWGCCTTYYKTRTACNAACTSGB 25
|||||:|||||:|:|||||:
Db 557 AGCCGTGCTTCTGTGTACAAACTCGT 581

RESULT 9					
CK212429					
LOCUS	CK212429	1062 bp	mRNA	linear	EST 09-DEC-2003
DEFINITION	FGAS024301	Triticum aestivum	FGAS: Library 6	CAP GATE 1	Triticum aestivum cDNA, mRNA sequence.

ESL.
KEYWORDS
SOURCE
ORGANISM

Triticum aestivum (bread wheat)
Triticum aestivum
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Triticum.

TITLE Functional Genomics of Abiotic Stress In Wheat and Canola Crops
JOURNAL Unpublished (2003)
COMMENT Contact: Wm L Crosby

Email: lgas.est@cs.ubask.ca
This sequence is the direct result of the Base calling software Phred (default parameters). It is the raw base calls. To aid in the identification of the high quality insert the software Lucy (default parameters) has been run on this sequence. Lucy identified the region [42..723].

FEATURES
SOURCE

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/mol_type="trxn:4565"
/db_xref="trxn:4565"
/clone_lib="Triticum aestivum FGAS: Library 6 CAP GATE 1"
/note="Organ: Crown and leaf; Vector: pCMV.SPORT; Crown
(50%) and leaf (50%) tissues from wheat cultivar Norstar
after short exposure times to low temperature in the light
and in the dark. 12 mRNA populations were combined before
constructing the library. The first 6 populations: After 7

```

days of growth at 20°Cs from wheat cultivar Norstar after short exposure times to low temperature in the light and in the dark. 12 mRNA populations were combined before constructing the library. The first 6 populations: After 7 days of growth at 20, wheat plants were transferred to 4°C in the light. 1cm crown sections and green leaf tissue were separately harvested after 1, 3, and 6 hours of low temperature exposure. The last 6 populations: After 7 days of growth at 20°C, wheat plants were transferred to 4°C in the dark. 1cm crown sections and green leaf tissue were separately harvested after 1, 3, and 6 hours of low temperature exposure. First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with NotI. In addition, this library used a primer for second strand synthesis that annealed to an artificial sequence (RNA oligo) added before first strand synthesis. Therefore when sequences from EST generated from this library will be masked for vector and adaptor sequences, an additional masking step will have to be included to mask this RNA oligo that is common to all clones (sequence CCACTGGAGCAGGACACTGCATGCTGACTGAGGAGTAGAAA)."

ORIGIN

Query Match 84.8%; Score 21.2; DB 7; Length 1062;
Best Local Similarity 72.0%; Pred. No. 24;
Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCCWGCCTTYYKTRTACNACTSG 25

|||||:|||||:|||||:|||||:

Db 791 AGCCTGCTTTTGTACAACTGGT 815

RESULT 10

CK212431

LOCUS

DEFINITION FGAS024303 Triticum aestivum mRNA linear EST 09-DEC-2003

aestivum cDNA, mRNA sequence.

CK212431

CK212431.1 GI:39618535

EST.

ORGANISM Triticum aestivum (bread wheat)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticeae; Triticum.

1 (bases 1 to 1067)

Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,D.,

Genswein,B., Graf,R., Gulick,P., Hrycan,L.D., Laroche,A.,

Links,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilsson,D.,

Penniket,C., Roach,J.L. and Sarhan,F.

Functional Genomics of Abiotic Stress In Wheat and Canola Crops

Unpublished (2003)

Contact: Wm L Crosby

Bioinformatics

University of Saskatchewan, Department of Computer Science

1C101 Engineering Building, 57 Campus Drive, Saskatoon,

Saskatchewan, S7N 5A9, Canada

Tel: 306 966 1769

Fax: 306 966 2033

Email: fgas_estseqs.usask.ca

This sequence is the direct result of the Base calling software

Phred (default parameters). It is the raw base calls. To aid in the

identification of the high quality insert the software Lucy

(default parameters) has been run on this sequence. Lucy identified

the region [22,802].

Plate: L6B005 row: K column: 05.

Location/Qualifiers

1..1067

/organism="Triticum aestivum"

/mol_type="mRNA"

/db_xref="caxon:4565"

/clone_lib="Triticum aestivum FGAS: Library 6 CAP GATE 1"

FEATURES

source

/note="Organ: Crown and leaf; Vector: pCMV.SP0RT6; Crown (50%) and leaf (50%) tissues from wheat cultivar Norstar after short exposure times to low temperature in the light and in the dark. 12 mRNA populations were combined before constructing the library. The first 6 populations: After 7 days of growth at 20°Cs from wheat cultivar Norstar after short exposure times to low temperature in the light and in the dark. 12 mRNA populations were combined before constructing the library. The first 6 populations: After 7 days of growth at 20, wheat plants were transferred to 4°C in the light. 1cm crown sections and green leaf tissue were separately harvested after 1, 3, and 6 hours of low temperature exposure. First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with NotI. In addition, this library used a primer for second strand synthesis that annealed to an artificial sequence (RNA oligo) added before first strand synthesis. Therefore when sequences from EST generated from this library will be masked for vector and adaptor sequences, an additional masking step will have to be included to mask this RNA oligo that is common to all clones (sequence CCACTGGAGCAGGACACTGCATGCTGACTGAGGAGTAGAAA)."

ORIGIN

Query Match 84.8%; Score 21.2; DB 7; Length 1067;
Best Local Similarity 72.0%; Pred. No. 24;
Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCCWGCCTTYYKTRTACNACTSG 25

|||||:|||||:|||||:|||||:

Db 871 AGCCTGCTTTTGTACAACTGGT 895

RESULT 11

CK213073

LOCUS

DEFINITION FGAS024975 Triticum aestivum FGAS: Library 6 CAP GATE 1 Triticum

aestivum cDNA, mRNA sequence.

CK213073

CK213073.1 GI:39619177

EST.

SOURCE Triticum aestivum (bread wheat)

ORGANISM Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticeae; Triticum.

1 (bases 1 to 1070)

Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,D.,

Genswein,B., Graf,R., Gulick,P., Hrycan,L.D., Laroche,A.,

Links,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilsson,D.,

Penniket,C., Roach,J.L. and Sarhan,F.

Functional Genomics of Abiotic Stress In Wheat and Canola Crops

Unpublished (2003)

Contact: Wm L Crosby

Bioinformatics

University of Saskatchewan, Department of Computer Science

1C101 Engineering Building, 57 Campus Drive, Saskatoon,

Saskatchewan, S7N 5A9, Canada

Tel: 306 966 1769

Fax: 306 966 2033

Email: fgas_estseqs.usask.ca

This sequence is the direct result of the Base calling software

Phred (default parameters). It is the raw base calls. To aid in the

identification of the high quality insert the software Lucy

(default parameters) has been run on this sequence. Lucy identified

the region [22,640].

Plate: L6B008 row: B column: 07.

Location/Qualifiers

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 /mol_type="mRNA"
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 /clone_lib="Triticum aestivum FGAS: Library 6 CAP GATE 1"
 /note="Organ: Crown and leaf; Vector: pCMV.SPORT6; Crown (50%) and leaf (50%) tissues from wheat cultivar Norstar after short exposure times to low temperature in the light and in the dark. 12 mRNA populations were combined before constructing the library. The first 6 populations: After 7 days of growth at 20°C from wheat cultivar Norstar after short exposure times to low temperature in the light and in the dark. 12 mRNA populations were combined before constructing the library. The first 6 populations: After 7 days of growth at 20, wheat plants were transferred to 4°C in the light. 1cm crown sections and green leaf tissue were separately harvested after 1, 3, and 6 hours of low temperature exposure. The last 6 populations: After 7 days of growth at 20°C, wheat plants were transferred to 4°C in the dark. 1cm crown sections and green leaf tissue were separately harvested after 1, 3, and 6 hours of low temperature exposure. First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with NotI. In addition, this library used a primer for second strand synthesis that annealed to an artificial sequence (RNA oligo) added before first strand synthesis. Therefore when sequences from EST generated from this library will be masked for vector and adaptor sequences, an additional masking step will have to be included to mask this RNA oligo that is common to all clones (sequence CGACTGGAGCAGGAGCAGTGCATGACTGAGGAGTAGAAA)."

ORIGIN

Query Match 84.8%; Score 21.2; DB 7; Length 1070;
 Best Local Similarity 72.0%; Pred. No. 24;
 Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTYYKTRTACNAACTSGB 25
 |||||:||||:||||:||||:||||:
 Db 675 AGCCTGCTTTTGTACAACTGCT 699

RESULT 12
 CK211886
 LOCUS
 DEFINITION FGAS023748 Triticum aestivum FGAS: Library 6 CAP GATE 1 Triticum aestivum cDNA, mRNA sequence.
 CK211886
 ACCESSION
 VERSION CK211886.1 GI:39617990
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum

REFERENCE
 AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.
 1 (bases 1 to 1071)
 Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D., Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroché, A., Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D., Penniket, C., Roach, J.L. and Sarhan, F.
 Functional Genomics of Abiotic Stress in Wheat and Canola Crops
 Unpublished (2003)
 Contact: Wm L Crosby
 Bioinformatics

TITLE
 JOURNAL
 COMMENT University of Saskatchewan, Department of Computer Science,
 1C101 Engineering Building, 57 Campus Drive, Saskatoon,
 Saskatchewan, S7N 5A9, Canada
 Tel: 306 966 1769
 Fax: 306 966 2033
 Email: fgas_est@cs.usask.ca
 This sequence is the direct result of the Base calling software
 Phred (default parameters). It is the raw base calls. To aid in the

identification of the high quality insert the software Lucy (default parameters) has been run on this sequence. Lucy identified the region [12,834].
 Plate: L6B003 row: L column: 24.
 Location/Qualifiers

FEATURES

source

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ORIGIN

Query Match 84.8%; Score 21.2; DB 7; Length 1071;
 Best Local Similarity 72.0%; Pred. No. 24;
 Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTYYKTRTACNAACTSGB 25
 |||||:||||:||||:||||:||||:
 Db 925 AGCCTGCTTTTGTACAACTGCT 949

RESULT 13

CK212465
 LOCUS
 DEFINITION FGAS024338 Triticum aestivum FGAS: Library 6 CAP GATE 1 Triticum aestivum cDNA, mRNA sequence.

CK212465
 ACCESSION
 VERSION CK212465.1 GI:39618569
 KEYWORDS EST.

SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum

REFERENCE
 AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.

1 (bases 1 to 1071)
 Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D., Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroché, A., Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D., Penniket, C., Roach, J.L. and Sarhan, F.
 Functional Genomics of Abiotic Stress in Wheat and Canola Crops
 Unpublished (2003)
 Contact: Wm L Crosby
 Bioinformatics

TITLE
 JOURNAL
 COMMENT University of Saskatchewan, Department of Computer Science,
 1C101 Engineering Building, 57 Campus Drive, Saskatoon,
 Saskatchewan, S7N 5A9, Canada

Tel: 306 966 1769
 Fax: 306 966 2033
 Email: fgas_estseqs.usask.ca
 This sequence is the direct result of the Base calling software
 Phred (default parameters). It is the raw base calls. To aid in the
 identification of the high quality insert the software Lucy
 (default parameters) has been run on this sequence. Lucy identified
 the region [57,669].
 Plate: L6B005 row: M column: 04.

FEATURES

Location/Qualifiers
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/organism="Triticum aestivum"
 /mol_type="mRNA"
 /db_xref="taxon:4565"
 /clone_lib="Triticum aestivum FGAS: Library 6 CAP GATE 1"
 /note="Organ: Crown and leaf; Vector: pCMV.SPORT6; Crown
 (50%) and leaf (50%) tissues from wheat cultivar Norstar
 after short exposure times to low temperature in the light
 and in the dark. 12 mRNA populations were combined before
 constructing the library. The first 6 populations: After 7
 days of growth at 20°Cs from wheat cultivar Norstar after
 short exposure times to low temperature in the light and
 in the dark. 12 mRNA populations were combined before
 constructing the library. The first 6 populations: After 7
 days of growth at 20, wheat plants were transferred to 4C
 in the light. 1cm crown sections and green leaf tissue were
 separately harvested after 1, 3, and 6 hours of low
 temperature exposure. The last 6 populations: After 7 days
 of growth at 20C, wheat plants were transferred to 4C in
 the dark. 1cm crown sections and green leaf tissue were
 separately harvested after 1, 3, and 6 hours of low
 temperature exposure. First strand synthesis in this
 library was done in the presence of methylated dCTP
 thereby protecting from internal cleavage with NotI. In
 addition, this library used a primer for second strand
 synthesis that annealed to an artificial sequence (RNA
 oligo) added before first strand synthesis. Therefore when
 sequences from EST generated from this library will be
 masked for vector and adaptor sequences, an additional
 masking step will have to be included to mask this RNA
 oligo that is common to all clones (sequence
 CGACTGGACGACGAGGACACTGACATGCTGAAGGAGTAGAAA)."

ORIGIN

Query Match 84.8%; Score 21.2; DB 7; Length 1071;
 Best Local Similarity 72.0%; Pred. No. 24;
 Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCCWGCCTTYYKTRTACNACTSGB 25
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 DB 738 AGCCTGCTTTTGTGACAACTGGT 762

RESULT 14
 CK216054
 LOCUS
 DEFINITION FGAS028031 Triticum aestivum FGAS: Library 6 CAP GATE 1 Triticum
 aestivum cDNA, mRNA sequence.
 ACCESSION CK216054
 VERSION CK216054.1 GI:39622158
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.
 1 (bases 1 to 1076)

REFERENCE
 AUTHORS Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,D.,
 Genswein,B., Graf,R., Gulick,F., Hrycan,L.D., Laroche,A.,
 Links,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilsson,D.,
 Penniket,C., Roach,J.L. and Sarhan,F.
 Functional Genomics of Abiotic Stress In Wheat and Canola Crops
 Unpublished (2003)

TITLE
 JOURNAL

COMMENT

Contact: Wm L Crosby
 Bioinformatics
 University of Saskatchewan, Department of Computer Science
 1C101 Engineering Building, 57 Campus Drive, Saskatoon,
 Saskatchewan, S7N 5A9, Canada
 Tel: 306 966 1769
 Fax: 306 966 2033
 Email: fgas_estseqs.usask.ca
 This sequence is the direct result of the Base calling software
 Phred (default parameters). It is the raw base calls. To aid in the
 identification of the high quality insert the software Lucy
 (default parameters) has been run on this sequence. Lucy identified
 the region [16,760].
 Plate: L6B020 row: L column: 02.

FEATURES

source

Location/Qualifiers

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 /db_xref="taxon:4565"
 /clone_lib="Triticum aestivum FGAS: Library 6 CAP GATE 1"
 /note="Organ: Crown and leaf; Vector: pCMV.SPORT6; Crown
 (50%) and leaf (50%) tissues from wheat cultivar Norstar
 after short exposure times to low temperature in the light
 and in the dark. 12 mRNA populations were combined before
 constructing the library. The first 6 populations: After 7
 days of growth at 20Cs from wheat cultivar Norstar after
 short exposure times to low temperature in the light and
 in the dark. 12 mRNA populations were combined before
 constructing the library. The first 6 populations: After 7
 days of growth at 20, wheat plants were transferred to 4C
 in the light. 1cm crown sections and green leaf tissue were
 separately harvested after 1, 3, and 6 hours of low
 temperature exposure. The last 6 populations: After 7 days
 of growth at 20C, wheat plants were transferred to 4C in
 the dark. 1cm crown sections and green leaf tissue were
 separately harvested after 1, 3, and 6 hours of low
 temperature exposure. First strand synthesis in this
 library was done in the presence of methylated dCTP
 thereby protecting from internal cleavage with NotI. In
 addition, this library used a primer for second strand
 synthesis that annealed to an artificial sequence (RNA
 oligo) added before first strand synthesis. Therefore when
 sequences from EST generated from this library will be
 masked for vector and adaptor sequences, an additional
 masking step will have to be included to mask this RNA
 oligo that is common to all clones (sequence
 CGACTGGACGACGAGGACACTGACATGCTGAAGGAGTAGAAA)."

ORIGIN

Query Match 84.8%; Score 21.2; DB 7; Length 1076;
 Best Local Similarity 72.0%; Pred. No. 24;
 Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCCWGCCTTYYKTRTACNACTSGB 25
 ||||:|||||:|||||:|||||:|||||:
 DB 822 AGCCTGCTTTTGTGACAACTGGT 846

RESULT 15

CK212170
 LOCUS
 DEFINITION FGAS024038 Triticum aestivum FGAS: Library 6 CAP GATE 1 Triticum
 aestivum cDNA, mRNA sequence.
 ACCESSION CK212170
 VERSION CK212170.1 GI:39618274
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.
 1 (bases 1 to 1082)
 REFERENCE
 AUTHORS Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,D.,

Genswein,B., Graf,R., Gulick,P., Hrycan,L.D., Laroche,A.,
 Links,M.G., McCarthy,E.B., Monroy,A., Muzak,I., Nilson,D.,
 Penniket,C., Roach,J.L. and Sarhan,F.
 Functional Genomics of Abiotic Stress In Wheat and Canola Crops
 Unpublished (2003)
 Contact: Wm L Crosby
 Bioinformatics

University of Saskatchewan, Department of Computer Science
 1C101 Engineering Building, 57 Campus Drive, Saskatoon,
 Saskatchewan, S7N 5A9, Canada

Tel: 306 966 1769
 Fax: 306 966 2033

Email: fgas_est@cs.usask.ca

This sequence is the direct result of the Base calling software
 Phred (default parameters). It is the raw base calls. To aid in the
 identification of the high quality insert the software Lucy
 (default parameters) has been run on this sequence. Lucy identified
 the region [39,712].

Plate: LEB004 row: L column: 06.

FEATURES source

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   Location/Qualifiers
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     .note="Organ: Crown and leaf; Vector: pCMV.SPORT6; Crown
(50%) and leaf (50%) tissues from wheat cultivar Norstar
after short exposure times to low temperature in the light
and in the dark. 12 mRNA populations were combined before
constructing the library. The first 6 populations: After 7
days of growth at 20C from wheat cultivar Norstar after
short exposure times to low temperature in the light and
in the dark. 12 mRNA populations were combined before
constructing the library. The first 6 populations: After 7
days of growth at 20, wheat plants were transferred to 4C
in the light. 1cm crown sections and green leaf tissu were
separately harvested after 1, 3, and 6 hours of low
temperature exposure. The last 6 populations: After 7 days
of growth at 20C, wheat plants were transferred to 4C in
the dark. 1cm crown sections and green leaf tissu were
separately harvested after 1, 3, and 6 hours of low
temperature exposure. First strand synthesis in this
library was done in the presence of methylated dCTP
thereby protecting from internal cleavage with NotI. In
addition, this library used a primer for second strand
synthesis that annealed to an artificial sequence (RNA
oligo) added before first strand synthesis. Therefore when
sequences from EST generated from this library will be
masked for vector and adaptor sequences, an additional
masking step will have to be included to mask this RNA
oligo that is common to all clones (sequence
CGACTGGAGCAGGACACTGTCATGCTGAGGAGTAGAAA)."

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ORIGIN

Query Match 84.8%; Score 21.2; DB 7; Length 1082;
 Best Local Similarity 72.0%; Pred. NO. 24;
 Matches 18; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTYYKTRTACNACTSGB 25

Db 815 AGCCTGCTTTTGTGTACNACTGGT 839

Search completed: November 16, 2004, 10:16:29
 Job time : 1534 secs

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JOURNAL Patent: US 6270969-A 3 07-AUG-2001;
 FEATURES Location/Qualifiers
 source 1..25
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTCKTRTACNAACTSG 25
 |||||
 DB 1 GTTCAGCTTCTCKTRTACNAACTSG 25

RESULT 3

AR493775 AR493775 25 bp mRNA linear PAT 15-MAY-2004
 DEFINITION Sequence 3 from patent US 6720140.
 ACCESSION AR493775
 VERSION AR493775.1 GI:47266186
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 25)
 AUTHORS Hartley, J.L. and Brasch, M.A.
 TITLE Recombinational cloning using engineered recombination sites
 JOURNAL Patent: US 6720140-A 3 13-APR-2004;
 FEATURES Location/Qualifiers
 source 1..25
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 /mol_type="mRNA"

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTCKTRTACNAACTSG 25
 |||||
 DB 1 GTTCAGCTTCTCKTRTACNAACTSG 25

RESULT 4

AX269133 AX269133 25 bp DNA linear PAT 29-OCT-2001
 LOCUS Sequence 4 from Patent WO0174861.
 DEFINITION AX269133
 ACCESSION AX269133
 VERSION AX269133.1 GI:16542053
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1
 AUTHORS Ville, R.G., Harrington, K., Murphy, S. and Bateman, A.
 TITLE Compositions and methods for tissue specific gene regulation
 JOURNAL therapy
 Patent: WO 0174861-A 4 11-OCT-2001;
 MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
 FEATURES Location/Qualifiers
 source 1..25
 /organism="synthetic construct"
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 /note="Synthetically generated vector sequence"

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTCKTRTACNAACTSG 25
 |||||
 DB 1 GTTCAGCTTCTCKTRTACNAACTSG 25

RESULT 5

AX491642 AX491642 25 bp DNA linear PAT 16-AUG-2002
 LOCUS Sequence 3 from Patent EP1227147.
 DEFINITION AX491642
 ACCESSION AX491642
 VERSION AX491642.1 GI:22324150
 KEYWORDS unidentified
 SOURCE unidentified
 ORGANISM unclassified.

REFERENCE 1
 AUTHORS Hartley, J.L. and Brasch, M.A.
 TITLE Recombinational cloning using engineered recombination sites
 JOURNAL Patent: EP 1227147-A 3 31-JUL-2002;
 INVITROGEN CORPORATION (US)
 FEATURES Location/Qualifiers
 source 1..25
 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"

ORIGIN

Query Match 88.0%; Score 22; DB 6; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTCKTRTACNAACTSG 25
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 DB 1 GTTCAGCTTCTCKTRTACNAACTSG 25

RESULT 6

AX498613 AX498613 25 bp DNA linear PAT 26-SEP-2002
 LOCUS Sequence 3 from Patent EP1229113.
 DEFINITION AX498613
 ACCESSION AX498613
 VERSION AX498613.1 GI:23343410
 KEYWORDS unidentified
 SOURCE unidentified
 ORGANISM unclassified.

REFERENCE 1
 AUTHORS Hartley, J.L. and Brasch, M.A.
 TITLE Recombinational cloning using engineered recombination sites
 JOURNAL Patent: EP 1229113-A 3 07-AUG-2002;
 INVITROGEN CORPORATION (US)
 FEATURES Location/Qualifiers
 source 1..25
 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"

ORIGIN

Query Match 88.0%; Score 22; DB 6; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTCKTRTACNAACTSG 25
 |||||
 DB 1 GTTCAGCTTCTCKTRTACNAACTSG 25

RESULT 7

BD131329 BD131329 25 bp DNA linear PAT 18-SEP-2002
 LOCUS Recombinational cloning using nucleic acids having recombination
 DEFINITION sites.
 ACCESSION BD131329

Query Match 84.8%; Score 21.2; DB 6; Length 25;
Best Local Similarity 76.0%; Pred. No. 5.1;

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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6720140-A 10 13-APR-2004;
FEATURES
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            /mol_type="mRNA"
ORIGIN
Query Match      83.2%; Score 20.8; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 8.3;
Matches 20; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTCKTRTACNAACTSGB 25
Db 1 GTTCAGCTTCTCTGTACAAACTTGT 25

RESULT 12
LOCUS AX491649 25 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 10 from Patent EP1227147.
ACCESSION AX491649
VERSION AX491649.1 GI:22324157
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1227147-A 10 31-JUL-2002;
INVITROGEN CORPORATION (US)
FEATURES
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ORIGIN

Query Match      83.2%; Score 20.8; DB 6; Length 25;
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Matches 20; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTCKTRTACNAACTSGB 25
Db 1 GTTCAGCTTCTCTGTACAAACTTGT 25

RESULT 13
LOCUS AX498620 25 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 10 from Patent EP1229113.
ACCESSION AX498620
VERSION AX498620.1 GI:233343417
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1229113-A 10 07-AUG-2002;
INVITROGEN CORPORATION (US)
FEATURES
    source      Location/Qualifiers
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"
ORIGIN

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Query Match      83.2%; Score 20.8; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 8.3;
Matches 20; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTCKTRTACNAACTSGB 25
Db 1 GTTCAGCTTCTCTGTACAAACTTGT 25

RESULT 14
LOCUS BD131336 25 bp DNA linear PAT 18-SEP-2002
DEFINITION Recombinational cloning using nucleic acids having recombination sites.
ACCESSION BD131336
VERSION BD131336.1 GI:23226281
KEYWORDS JP 2002500861-A/10.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE Recombinational cloning using nucleic acids having recombination sites
JOURNAL Patent: JP 2002500861-A 10 15-JAN-2002;
LIFE TECHNOLOGIES INC
COMMENT OS Unknown
PN JP 2002500861-A/10
PD 15-JAN-2002
PF 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 P1
JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC
C12N15/09, C12O1/68, C12N15/00
CC Description of Unknown Organism: recombination products FH
Key source      Location/Qualifiers
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FEATURES
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            /db_xref="taxon:32644"
ORIGIN

Query Match      83.2%; Score 20.8; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 8.3;
Matches 20; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTCKTRTACNAACTSGB 25
Db 1 GTTCAGCTTCTCTGTACAAACTTGT 25

RESULT 15
LOCUS BD263260 43 bp DNA linear PAT 17-JUL-2003
DEFINITION Compositions and methods for use in recombinational cloning of nucleic acids.
ACCESSION BD263260
VERSION BD263260.1 GI:33073028
KEYWORDS JP 2002537790-A/38.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 43)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
TITLE Compositions and methods for use in recombinational cloning of nucleic acids
JOURNAL Patent: JP 2002537790-A 38 12-NOV-2002;
INVITROGEN CORP
COMMENT OS Artificial Sequence
PN JP 2002537790-A/38
PD 12-NOV-2002

```

PF 02-MAR-2000 JP 2000602252
 PR 02-MAR-1999 US 60/122389, 23-MAR-1999 US 60/126049 PR
 28-MAY-1999 US 60/136744
 PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC
 C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/ PC
 00, C12N5/00
 CC attr2

FEATURES
 source
 FH Key Location/Qualifiers
 FT source 1..43
 FT source /organism='Artificial Sequence'.
 Location/Qualifiers
 1..43
 /organism='synthetic construct'
 /mol_type='genomic DNA'
 /db_xref='taxon:32630'

ORIGIN

Query Match 83.2%; Score 20.8; DB 6; Length 43;
 Best Local Similarity 80.0%; Pred. No. 8.4;
 Matches 20; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 GTTCAGCTTTCTKTRTACNAACTSGB 25
 |||||:||||:||||:||||:
 Db 29 GTTCAGCTTTCTTGTACAACTTGT 5

Search completed: November 16, 2004, 06:01:00
 Job time : 709.5 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:29:13 ; Search time 167.8 Seconds
(without alignments)
782.095 Million cell updates/sec

Title: US-10-820-133-3

Perfect score: 25

Sequence: 1 gttcagctttcttactnaactsgb 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 413486 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_23Sep04.*
1: geneseqn1980s.*
2: geneseqn1990s.*
3: geneseqn2000s.*
4: geneseqn2001as.*
5: geneseqn2001bs.*
6: geneseqn2002as.*
7: geneseqn2002bs.*
8: geneseqn2003as.*
9: geneseqn2003bs.*
10: geneseqn2003cs.*
11: geneseqn2003ds.*
12: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	88.0	25	2	AAT48212
2	22	88.0	25	2	AAX78937
3	22	88.0	25	4	AAC87868
4	22	88.0	25	4	AAX78937
5	22	88.0	25	4	AAD14431
6	22	88.0	25	5	AAS14782
7	22	88.0	25	8	ABT16623
8	22	88.0	25	9	ACD28278
9	22	88.0	25	9	ACD28478
10	22	88.0	25	9	ADA38164
11	22	88.0	25	10	AAD60560
12	22	88.0	25	10	ACC44652
13	22	88.0	25	12	ADL93418
14	21.2	84.8	25	2	AAX78937
15	20.8	83.2	25	2	AAT48219
16	20.8	83.2	25	2	AAX78944
17	20.8	83.2	25	4	AAC87875
18	20.8	83.2	25	4	AAX78937
19	20.8	83.2	25	4	AAX78937
20	20.8	83.2	25	6	ABT16623
21	20.8	83.2	25	8	ABT16629

22	20.8	83.2	25	9	ACD28285
23	20.8	83.2	25	9	ACD28485
24	20.8	83.2	25	9	ADA38171
25	20.8	83.2	25	10	AAD60567
26	20.8	83.2	25	10	ACC44659
27	20.8	83.2	25	12	ADL93425
28	20.8	83.2	25	13	AAS55546
c	20.8	83.2	43	3	AAS55546
c	20.8	83.2	43	4	AAS06218
30	20.4	81.6	25	2	AAX78945
31	20.4	81.6	25	4	AAS06185
32	20.4	81.6	25	10	ABZ58738
33	20.4	81.6	25	10	ACC59582
34	20.4	81.6	25	12	ADJ46356
35	20.4	81.6	25	12	ADO06650
c	20.4	81.6	25	12	ADQ48458
37	20.4	81.6	37	12	ADH48079
38	20.4	81.6	102	3	AAC55509
39	20.4	81.6	102	3	AAC55512
40	20.4	81.6	135	3	AAC55385
41	20.4	81.6	153	3	AAC55506
42	20.4	81.6	158	10	ADF42425
43	20.4	81.6	204	3	AAC55463
44	20.4	81.6	1846	6	AAD44626
45	20.4	81.6	4554	3	AAC55541

ALIGNMENTS

RESULT 1

AAT48212

ID AAT48212 standard; DNA; 25 BP.

XX AC AAT48212;

XX DT 20-OCT-1997 (first entry)

XX DE M-attr core region.

XX KW att recombination site; core region; mutation; enhance; recombination;

XX OS Synthetic.

XX PN WO9640724-A1.

XX PD 19-DEC-1996.

XX PF 07-JUN-1996; 96WO-US010082.

XX PR 07-JUN-1995; 95US-00486139.

XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Hartley JL, Brasch MA;

XX DR WPI; 1997-065168/06.

XX PT Nucleic acids, vectors and methods to obtain chimeric nucleic acid -

XX PT using recombinant proteins and engineered recombination sites in vitro or

XX PS in vivo.

XX PS Claim 14; Page 55; 106pp; English.

XX CC AAT48210-25 are att recombination site core region DNA sequences. The

XX CC core region has at least one engineered mutation that enhances

XX CC recombination in vitro in the formation of a Cointegrate or Product DNA.

XX CC These core regions can be incorporated into novel vector donor DNA

XX CC molecules. The nucleic acids, vectors and methods of the invention are

XX CC used to obtain chimeric nucleic acid using recombination proteins and

XX CC engineered recombination sites in vitro or in vivo. The improved

XX CC specificity, speed and yields of the invention facilitates DNA or RNA

XX CC subcloning, regulation or exchange useful for any related purpose, e.g.

CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
CC or modification of transcribed, replicated, isolated or genomic DNA or
CC RNA

XX Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 5 Other;

Query Match 88.0%; Score 22; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTKTRTACNACTSGB 25
|||||
Db 1 GTTCAGCTTCTKTRTACNACTSGB 25

RESULT 2

AAx78937
ID AAX78937 standard; DNA; 25 BP.

XX
AC AAX78937;

XX 17-AUG-1999 (first entry)

XX Oligonucleotide #3 for recombination and cloning method.

XX Cloning; donor; recombination site; vector; chimeric; ss.

XX Synthetic.

XX WO9921977-A1.

XX 06-MAY-1999.

XX 26-OCT-1998; 98WO-US022589.

XX 24-OCT-1997; 97US-0065930P.

XX 23-OCT-1998; 98US-00177387.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Fox DK;

XX WPI; 1999-303011/25.

XX New nucleic acid cloning methods.

XX Disclosure; Page 159; 195pp; English.

CC The invention relates to novel methods for cloning or subcloning one or
CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
CC more desired nucleic acid segments flanked by at least 2 recombination
CC sites which do not recombine with each other; (2) one or more vector
CC donor molecules (VDMs) comprising at least 2 recombination sites which do
CC not recombine with each other; and (3) one or more site-specific
CC recombination proteins; (b) incubating the combination to transfer one or
CC more of the desired segments into one or more of the VDMs, thereby
CC producing one or more desired product molecules (PWMs). The methods can be
CC used for the efficient and specific recombination of NAM segments. They
CC can be used to generate chimeric DNA or RNA molecules that have the
CC desired characteristics and/or nucleic acid segments. The methods can
CC also be used for changing vectors. The oligonucleotides AAX78935-X78994
CC are used in the method of the invention

XX Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 5 Other;

Query Match 88.0%; Score 22; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTKTRTACNACTSGB 25
|||||
Db 1 GTTCAGCTTCTKTRTACNACTSGB 25

RESULT 3

AAC87868

ID AAC87868 standard; DNA; 25 BP.

XX
AC AAC87868;

XX 02-MAR-2001 (first entry)

XX Escherichia coli core region recombinant site m-attr SEQ ID NO:3.

XX Core region; recombination site; cloning; chimeric DNA; characteristic;
XX mutation; att site; lox site; ss.

XX Escherichia coli.

XX US6143557-A.

XX 07-NOV-2000.

XX 20-JAN-1999; 99US-00233493.

XX 07-JUN-1995; 95US-00486139.

XX 07-JUN-1996; 96US-00663002.

XX 12-JAN-1998; 98US-00005476.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Brasch MA, Hartley JL;

XX WPI; 2001-049004/06.

XX Isolated nucleic acid molecules comprising a DNA segment having two
XX engineered recombination sites, derived from att or lox, which flank a
XX selectable marker and comprise a core region having an engineered
XX mutation.

XX Claim 1; Col 18; 73pp; English.

XX The present invention describes an isolated nucleic acid molecule (I)
XX comprising a first nucleic acid sequence having a defined sequence
XX (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,
XX or an RNA sequence corresponding to AAC87866 to AAC87881. Also described
XX are: (1) an isolated nucleic acid molecule (II) comprising a first
XX mutated recombination site that removes one or more stop codons from the
XX recombination site or avoids hairpin formation, the recombination site
XX being an att or lox site; (2) an isolated nucleic acid molecule (III)
XX comprising a first att recombination site comprising a mutation that
XX enhances recombination specificity; (3) vectors (IV) comprising the above
XX mentioned nucleic acids; and (4) cells comprising the above mentioned
XX nucleic acids or (IV). The nucleic acids are used in engineering a core
XX region of a given recombination site to provide mutative sites suitable
XX for subcloning reactions. The use of nucleic acids for obtaining
XX engineered recombination in vitro or in vivo makes the methods for DNA or
XX RNA subcloning, highly specific, rapid, and less labour intensive

XX Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 5 Other;

Query Match 88.0%; Score 22; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTKTRTACNACTSGB 25
|||||
Db 1 GTTCAGCTTCTKTRTACNACTSGB 25

RESULT 4

AAF55737

ID AAF55737 standard; DNA; 25 BP.

XX
AC AAF55737;

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XX 12-APR-2001 (first entry)
DT Recombination site m-attr.
DE Recombination site; cloning; m-att; ss.
XX Unidentified.
XX US6171861-B1.
XX 09-JAN-2001.
XX 12-JAN-1998; 98US-00005476.
XX 07-JUN-1995; 95US-00486139.
XX 07-JUN-1996; 96US-00663002.
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX Hartley JL, Brasch MA;
XX WPI; 2001-136877/14.
XX In vitro cloning of nucleic acid involves mixing vectors comprising
PT recombination sites and/or nucleic acid, incubating mixture to produce
PT chimeric molecule, contacting hosts with mixture and selecting host.
XX Claim 24; Col 46; 73pp; English.
XX The present invention relates to a method for in vitro cloning of a
CC nucleic acid of interest. The method involves mixing in vitro two vectors
CC each comprising at least one recombination site and the nucleic acid of
CC interest; incubating the mixture in the presence of at least one
CC recombination protein to result in recombination of the recombination
CC sites, leading to production of a chimeric nucleic acid molecule
CC comprising the nucleic acid of interest; contacting hosts with the
CC mixture; and selecting for a host comprising the chimeric nucleic acid
CC molecule, and selecting against a host comprising the vectors comprising
CC the second vector, to clone the nucleic acid. The present sequence is a
CC recombination site, which may be used in the method of the present
CC invention
XX SQ Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 5 Other;
Query Match 88.0%; Score 22; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTTCAGCTTTCKTRTACNAACTSGB 25
Db 1 GTTCAGCTTTCKTRTACNAACTSGB 25
RESULT 5
AADI4431
ID AAD14431 standard; DNA; 25 BP.
XX AAD14431;
XX 01-NOV-2001 (first entry)
XX Recombination site m-attr DNA.
XX Recombination site; copy number; replicon; recombinatorial cloning;
XX m-attr; ds.
XX Unidentified.
XX US6270969-B1.
XX 07-AUG-2001.
XX

PF 20-JAN-1999; 99US-00233492.
XX 07-JUN-1995; 95US-00486139.
PR 07-JUN-1996; 96US-00663002.
XX (INVI-) INVITROGEN CORP.
XX Hartley JL, Brasch MA;
XX WPI; 2001-488248/53.
XX Methods for apposing nucleic acids comprising an expression signal and a
PT gene/partial gene, using recombinatorial cloning by incubating the
PT nucleic acids in the presence of a recombination protein under conditions
PT for recombination.
XX Claim 14; Col 18; 76pp; English.
XX The invention relates to a method for apposing an expression signal and a
CC gene or partial gene, using recombinatorial cloning. The method incubates
CC nucleic acids comprising the expression signal and the gene/partial gene
CC in the presence of a recombination protein under conditions sufficient to
CC cause recombination and therefore appose the expression signal and the
CC gene or partial gene. The methods are useful for apposing an expression
CC signal and a gene or partial gene using recombinatorial cloning. The
CC methods are also useful for changing vectors, constructing genes for
CC fusion proteins, changing copy number, changing replicons, cloning into
CC phages, and cloning e.g., PCR products (with an attB site at one end and
CC a loxP site at the other end), genomic DNAs, and cDNAs. The methods are
CC highly specific, rapid, and less labour intensive than prior art methods.
CC The present sequence is a recombination site useful for recombination
CC cloning
XX SQ Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 5 Other;
Query Match 88.0%; Score 22; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTTCAGCTTTCKTRTACNAACTSGB 25
Db 1 GTTCAGCTTTCKTRTACNAACTSGB 25
RESULT 6
AAS14782
ID AAS14782 standard; DNA; 25 BP.
XX AAS14782;
XX 27-FEB-2002 (first entry)
XX Lambda phage Int recombinase site core region DNA sequence m-attr.
XX Recombinant nucleic acid vector; carcinoembryonic antigen; CEA; cytokine;
XX syncytium-inducing polypeptide; fusogenic membrane glycoprotein; tumour;
XX recombinase; tumour-specific promoter; hypoxic response element; HRE; ss;
XX tyrosinase promoter; Cre; FLP; retroviral vector; malignant cell; cancer;
XX cytostatic; gene therapy; Int recombinase site core region; m-attr;
XX excisive recombination.
XX Bacteriophage lambda.
XX WO200174861-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US010250.
XX 31-MAR-2000; 2000US-0193977P.
XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
XX

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PI Vile RG, Harrington K, Murphy S, Bateman A;
XX WPI; 2001-656985/75.
XX Recombinant nucleic acid vector for reducing tumor size, has expression
PT cassette comprises a promoter linked to nucleic acid sequence encoding a
PT syncytium-inducing polypeptide and flanked on either side by recombinase.
XX Disclosure; Page 42; 84pp; English.
XX The invention relates to a recombinant nucleic acid vector comprising a
CC first expression cassette, comprising a first promoter operably linked to
CC a nucleic acid sequence encoding a syncytium-inducing polypeptide (such
CC as a fusogenic membrane glycoprotein) and flanked on either side by a
CC sequence recognised by a recombinase, and/or a second expression cassette
CC comprising a tumour-specific promoter operably linked to a nucleic acid
CC sequence encoding a recombinase. The nucleic acid of the first expression
CC cassette may be linked to a hypoxic response element (HRE), the second
CC expression cassette may contain a promoter linked to a nucleic acid
CC encoding a cytokine, and a third cassette may contain a tumour specific
CC promoter linked to the nucleic acid encoding the recombinase. The tumour
CC specific promoter is, for example, a carcinoembryonic antigen (CEA)
CC promoter or a tyrosinase promoter and the recombinase is, for example,
CC Cre recombinase or Flp recombinase. The invention is useful for reducing
CC tumour size by administering the compositions as retroviral vectors, or
CC in a cell containing the vector, to an individual in need of treatment
CC for a disease caused by malignant cells. This sequence represents an Int
CC recombinase site core region m-attr, required for exsive recombination
XX
SQ Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 5 Other;

Query Match      88.0%; Score 22; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCCKRTACNAACTSGB 25
DB 1 GTTCAGCTTTCCKRTACNAACTSGB 25

RESULT 7
ABT16623
ID ABT16623 standard; DNA; 25 BP.
XX AC ABT16623;
XX
DT 03-APR-2003 (first entry)
XX Artificial plant chromosome related oligo SEQ ID No 35.
XX
KW Plant artificial chromosome; PAC; transgenic plant; vaccine;
KW blood factor; herbicide; stress; agronomical; nutrient quality;
KW bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
KW ds.
XX
OS Unidentified.
XX
PN WO200296923-A1.
XX
PD 05-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-US017451.
XX
PR 30-MAY-2001; 2001US-0294687P.
PR 04-JUN-2001; 2001US-0296329P.
XX
XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
PA (AGRI-) AGRISOMA INC.
XX
PI Perez C, Fabijanski SF, Perkins E;
XX WPI; 2003-140436/13.
XX

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PT Producing artificial chromosome by introducing a nucleic acid into plant
PT cell, selecting artificial chromosome that has one or more repeat regions
PT with equivalent amounts of euchromatic and heterochromatic nucleic acids.
XX Disclosure; Page 261; 269pp; English.
XX The invention relates to a novel method for producing plant artificial
CC chromosomes. The invention also relates to methods for targeting
CC insertion of heterologous DNA into plant artificial chromosomes, methods
CC for delivery of plant chromosomes to selected cells and tissues. The
CC isolated plant artificial chromosome (PAC) is useful for producing a
CC transgenic plant, which involves introducing the PAC into a plant cell.
CC The PAC comprises a heterologous nucleic acid encoding a gene product
CC such as enzymes, antisense RNA, rDNA, structural proteins, marker
CC proteins, ligands, receptors, ribozymes, therapeutic proteins, and
CC biopharmaceutical proteins, vaccines, blood factors, antigens, hormones,
CC cytokines, growth factors, antibodies, or a product that provides for
CC resistance to diseases, insects, herbicides, or stress in a plant. The
CC heterologous nucleic acid optionally encodes a product that provides an
CC agronomically important trait in the plant, e.g. a product that alters
CC nutrient use and/or improves the nutrient quality of the plant. The
CC heterologous nucleic acid is contained within a bacterial artificial
CC chromosome (BAC) or a yeast artificial chromosome (YAC). This
CC polynucleotide sequence represents an oligo relating to the method for
CC producing plant artificial chromosomes of the invention
XX
SQ Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 5 Other;

Query Match      88.0%; Score 22; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCCKRTACNAACTSGB 25
DB 1 GTTCAGCTTTCCKRTACNAACTSGB 25

RESULT 8
ACD28278
ID ACD28278 standard; DNA; 25 BP.
XX AC ACD28278;
XX
DT 02-OCT-2003 (first entry)
XX Nucleic acid core region m-attr.
XX Core region; ds; vector donor DNA; flanking recombination site; m-attr.
XX Synthetic.
XX US2003064515-A1.
PD 03-APR-2003.
XX
PF 30-JAN-2002; 2002US-00058291.
XX
PR 07-JUN-1995; 95US-00486139.
PR 07-JUN-1996; 96US-00663002.
PR 20-JAN-1999; 99US-00233493.
PR 02-NOV-1999; 99US-00432085.
XX
XX (HART/) HARTLEY J L.
PA (BRAS/) BRASCH M A.
XX
PI Hartley JL, Brasch MA;
XX
XX WPI; 2003-540791/51.
XX
XX New Vector Donor DNA molecule for recombinational cloning using
PT engineered recombination sites, comprises first and second DNA segments
PT that do not recombine with each other and that contain a Selectable
PT marker.

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XX Claim 14; Page 25; 71pp; English.

XX The invention relates to a vector donor DNA molecule comprising a first

CC DNA segment and a second DNA segment containing at least one selectable

CC marker. The first and second segments are separated either by, in a

CC circular vector donor, a first and a second recombination site, or in a

CC linear vector donor, at least a first recombination site, where each pair

CC of flanking recombination sites are engineered and do not recombine with

CC each other. The nucleic acid molecule, vectors and methods are useful for

CC moving or exchanging segments of DNA molecules using engineered

CC recombination sites and recombination proteins to provide chimeric DNA

CC molecules that have the desired characteristic(s) and/or DNA segment(s).

CC The present sequence represents the nucleic acid core region m-attr

XX Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 5 Other;

XX Query Match 88.0%; Score 22; DB 9; Length 25;

XX Best Local Similarity 100.0%; Pred. No. 0.86;

XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTKTRTACNAACTSGB 25

Db 1 GTTCAGCTTCTKTRTACNAACTSGB 25

RESULT 9

ACD28478

ID ACD28478 standard; DNA; 25 BP.

XX AC

AC ACD28478;

XX DT 09-OCT-2003 (first entry)

XX DE Nucleic acid core sequence m-attr.

XX KW Nucleic acid core; m-attr; cointegrate DNA; flanking recombination site;

XX KW ds.

XX OS Synthetic.

XX US2003068799-A1.

XX PD 10-APR-2003.

XX PF 06-JUN-2002; 2002US-00162879.

XX PR 07-JUN-1995; 95US-00486139.

XX PR 07-JUN-1996; 96US-00563002.

XX PR 20-JAN-1999; 99US-00233493.

XX PR 02-NOV-1999; 99US-00432085.

XX PA (INVI-) INVITROGEN CORP.

XX PI Hartley JL, Brasch MA;

XX WPI; 2003-540884/51.

XX Making Cointegrate DNA molecule, by combining recombination sites

PT flanking the desired DNA segment in insert donor DNA, with the

PT recombination sites of vector donor DNA, using site specific

PT recombination protein.

XX Claim 14; Page 25; 71pp; English.

XX The invention relates to a method of making a cointegrate DNA molecule.

CC The method is useful for making a cointegrate DNA molecule. The method is

CC useful for a variety of DNA exchanges, such as subcloning of DNA, in

CC vitro or in vivo. The method enables efficient and specific recombination

CC of DNA segments using recombination proteins. The method is highly

CC specific, rapid and less labour intensive. The improved specificity,

CC yield and speed of the method facilitates DNA or RNA subcloning,

CC regulation and exchange useful for other related purposes. Since single

CC molecules of the recombinations product can be introduced into a

CC biological host, propagation of the desired product DNA in the absence of

CC other DNA molecules is more readily realised. Reaction conditions can be

CC freely adjusted in vitro to optimise enzyme activities. The present

CC sequence represents the nucleic acid core sequence m-attr

XX Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 5 Other;

XX Query Match 88.0%; Score 22; DB 9; Length 25;

XX Best Local Similarity 100.0%; Pred. No. 0.86;

XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTKTRTACNAACTSGB 25

Db 1 GTTCAGCTTCTKTRTACNAACTSGB 25

RESULT 10

ADA38164

ID ADA38164 standard; DNA; 25 BP.

XX AC

AC ADA38164;

XX DT 20-NOV-2003 (first entry)

XX DE m-attr DNA sequence indicating generic core region of an attR site.

XX KW engineered recombination site; cloning; recombinase; subcloning; attB;

XX KW attP; attL; attR; selectable marker; cointegrate; m-attr; ds.

XX OS Synthetic.

XX US2003054552-A1.

XX PD 20-MAR-2003.

XX PF 30-JAN-2002; 2002US-00058292.

XX PR 07-JUN-1995; 95US-00486139.

XX PR 07-JUN-1996; 96US-00563002.

XX PR 20-JAN-1999; 99US-00233493.

XX PR 02-NOV-1999; 99US-00432085.

XX PA (HARTLEY) HARTLEY J L.

XX PA (BRASCH) BRASCH M A.

XX PI Hartley JL, Brasch MA;

XX WPI; 2003-585168/55.

XX New Vector Donor DNA molecule, useful for recombinational cloning

PT purposes, comprises a first and a second DNA segment that contains a

PT selectable marker and is separated by a pair of flanking, engineered

PT recombination sites.

XX Claim 14; Page 26; 72pp; English.

XX This invention relates to novel DNA and vectors having engineered

CC recombination sites for use in a cloning method that enables efficient

CC and specific recombination of DNA segments using recombination proteins

CC including recombinases. As such, it provides a method for obtaining

CC chimeric nucleic acids with the desired characteristics, facilitating DNA

CC or RNA subcloning, regulation and/or exchange. The recombination site is

CC derived from attB attP, attL or attR, where the att site is att1, att2 or

CC att3. Engineered mutations of the att sites (either one or multiple

CC mutations) can enhance specificity or efficiency of the recombination

CC reaction and the properties of the product DNA molecules. Accordingly,

CC the present invention describes a nucleic acid molecule comprising at

CC least one DNA segment having at least two engineered recombination sites

CC flanking a selectable marker and/or a desired DNA segment. Furthermore,

CC at least one of the engineered sites must enhance recombination in vitro

CC to form a cointegrate or product DNA molecule. This oligonucleotide

CC sequence is m-attr, a generic DNA sequence indicating the core region of

```

CC an attR recombination site of the invention.
XX Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 5 Other;
SQ

Query Match      88.0%; Score 22; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTKTRTACNAACTSG 25
Db 1 GTTCAGCTTTCTKTRTACNAACTSG 25

RESULT 11
AAD60560
ID AAD60560 standard; DNA; 25 BP.
XX
XX
AC AAD60560;
XX
DT 18-DEC-2003 (first entry)
XX
DE Core region DNA, m-attr.
XX
XW Recombinational cloning; DNA exchange; core region; ds.
XX
XX Unidentified.
OS
XX
PN US2003100110-A1.
XX
PD 29-MAY-2003.
XX
XX 02-NOV-1999; 99US-00432085.
PF
XX 07-JUN-1995; 95US-00486139.
PR
XX 07-JUN-1996; 96US-00663002.
PR
XX 20-JAN-1999; 99US-00233493.
XX
XX (HARTLEY J L.
PA (BRAS/) BRASCH M A.
XX
XX Hartley JL, Brasch MA;
PI
XX WPI; 2003-730143/69.
XX
XX New Vector Donor DNA molecule for recombinational cloning using
PT engineered recombination sites, comprises first and second DNA segments
PT that do not recombine with each other and that contain a Selectable
PT marker.
XX
PS Claim 14; Page 25; 71pp; English.
XX
XX The invention relates to a vector donor DNA molecule which comprises
CC first and second DNA segments that do not recombine with each other and
CC that contain a selectable marker. The invention also relates to a method
CC for recombinational cloning using engineered recombination sites. The
CC invention is useful for moving or exchanging segments of DNA molecules
CC using engineered recombination sites and recombination proteins to
CC provide chimeric DNA molecules that have the desired characteristic(s)
CC and/or DNA segment(s). The present sequence is a core region DNA. This
CC sequence is used to illustrate the method of the invention
XX
SQ Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 5 Other;
Query Match      88.0%; Score 22; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTKTRTACNAACTSG 25
Db 1 GTTCAGCTTTCTKTRTACNAACTSG 25

RESULT 12

```

```

ACC44652
ID ACC44652 standard; DNA; 25 BP.
XX
XX ACC44652;
AC
XX 29-MAY-2003 (first entry)
DT
XX Recombination site related oligonucleotide SEQ ID NO:43.
DE
XX Chromosome-based platform; artificial chromosome; eukaryotic chromosome;
KW att site; integrase; recombinase; ACes; gene therapy; transgenic animal;
KW platform artificial chromosome expression system; PCR primer; ss.
XX
XX Synthetic.
OS
XX WO200297059-A2.
PN
XX
XX 05-DEC-2002.
PD
XX 30-MAY-2002; 2002WO-US017452.
XX
PF 30-MAY-2001; 2001US-0294758P.
PR
XX 21-MAR-2002; 2002US-0366891P.
PR
XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
PA
XX Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;
PI Stewart S, Shellard J;
XX
XX WPI; 2003-140461/13.
XX
XX Novel eukaryotic chromosome comprising one or many att sites which
PT permits site-directed integration in the presence of lambda-integrase,
PT useful for site-specific recombination-directed integration of DNA of
PT interest.
XX
PS Claim 43; Page 143; 272pp; English.
XX
XX The present invention describes a eukaryotic chromosome (I) comprising
CC one or several att sites, where an att site is heterologous to the
CC chromosome, and permits site-directed integration in the presence of
CC lambda-integrase. Also described: (i) a platform artificial chromosome
CC expression system (ACes) (II) comprising several sites that participate
CC in recombinase catalysed recombination; and (2) a method (M1) for
CC introducing a heterologous nucleic acid into a platform artificial
CC chromosome. (I) can be used in gene therapy. (M1) is useful for
CC introducing a heterologous nucleic acid molecule into a platform
CC artificial chromosome, preferably an ACes. (II) is useful for producing a
CC transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or
CC mammal) by introducing (II) by cell fusion, lipid-mediated transfection,
CC by a carrier system, microinjection, microcell fusion, electroporation,
CC microprojectile bombardment or direct DNA transfer into an embryonic
CC cell, preferably a stem cell or an embryo. (II) comprises a heterologous
CC nucleic acid that encodes a therapeutic product which is useful for
CC making a library of ACes comprising random portions of a genome. ACC44612
CC to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 5 Other;
Query Match      88.0%; Score 22; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTKTRTACNAACTSG 25
Db 1 GTTCAGCTTTCTKTRTACNAACTSG 25

RESULT 13
ADL93418
ID ADL93418 standard; DNA; 25 BP.
XX

```

AC ADL93418;
 DT 01-JUL-2004 (first entry)
 XX
 DE Recombination site core region mutant m-attR.
 XX
 KW recombination protein; recombination site; Insert Donor DNA;
 KW Vector Donor DNA; repression cassette; DNA cloning;
 KW recombination site core region; ds; m-attR; mutant.
 XX
 OS Unidentified.
 OS Synthetic.
 XX US6720140-B1.
 XX
 PD 13-APR-2004.
 XX
 XX 04-FEB-2000; 2000US-00498074.
 XX
 PF 07-JUN-1995; 95US-00486139.
 PR 07-JUN-1996; 96US-00663002.
 PR 12-JAN-1998; 98US-00005476.
 XX
 XX (INVI-) INVITROGEN CORP.
 XX
 XX Hartley JL, Brasch MA;
 XX WPI; 2004-313648/29.
 XX
 XX New composition comprising recombination proteins and isolated nucleic
 PT acid molecule comprising recombination site, useful for moving or
 PT exchanging segments of DNA molecules to provide chimeric DNA molecules.
 XX
 XX Claim 8; SEQ ID NO 3; 80pp; English.
 XX
 XX The invention describes a composition comprising recombination proteins
 CC and an isolated nucleic acid molecule comprising a recombination site.
 CC The composition comprises one or more isolated recombination proteins and
 CC at least one Insert Donor DNA molecule comprising: at least a first
 CC recombination site, containing at least one mutation, where the mutation
 CC removes one or more stop codons from the recombination site and avoids
 CC hairpin formation; a first recombination site and a second recombination
 CC site where the first and second recombination sites do not recombine with
 CC each other, and at least one Vector Donor DNA molecule comprising a first
 CC recombination site and a second recombination site, where the first and
 CC second recombination sites do not recombine with each other. The Vector
 CC Donor DNA molecule comprises a repression cassette encoding a repressor
 CC and a selectable marker that is repressed by the repressor where the
 CC selectable marker and the repression cassette are on different DNA
 CC segments separated from each other by at least one recombination site; at
 CC least a first recombination site containing at least one nucleic acid
 CC sequence selected from a nucleic acid sequence that is 80-99% homologous
 CC to one or more of a nucleic acid sequence comprising 25 bp (SEQ ID NO. 1-
 CC 16). Also described are: a kit for in vitro cloning of DNA segments
 CC comprising one or more isolated recombination proteins and at least one
 CC Insert Donor DNA molecule; a method for in vitro cloning; a method for
 CC making a reaction mixture; and a reaction mixture made by the method
 CC above. The compositions, methods and kits of the invention are useful for
 CC moving or exchanging segments of DNA molecules using engineered
 CC recombination sites and recombination proteins to provide chimeric DNA
 CC molecules that have the desired characteristics and/or DNA segments. This
 CC sequence represents mutant recombination site core region m-attR that can
 CC be used in the composition of the invention.
 XX
 XX Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 5 Other;
 SQ
 Query Match 88.0%; Score 22; DB 12; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.86;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GTTCAGCTTCTCKTRTACNAACTSGB 25
 |||||||
 Db 1 GTTCAGCTTCTCKTRTACNAACTSGB 25
 |||||||

RESULT 14
 AAX78976
 ID AAX78976 standard; DNA; 25 BP.
 XX
 AC AAX78976;
 XX
 DT 17-AUG-1999 (first entry)
 XX
 DE Oligonucleotide #42 for recombination and cloning method.
 XX
 KW Cloning; donor; recombination site; vector; chimeric; ss.
 XX
 OS Synthetic.
 OS
 PN WO9921977-A1.
 XX
 PD 06-MAY-1999.
 XX
 XX 26-OCT-1998; 98WO-US022589.
 PF
 XX 24-OCT-1997; 97US-0065930P.
 PR
 PR 23-OCT-1998; 98US-00177387.
 XX
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 XX Hartley JL, Brasch MA, Temple GF, Fox DK;
 XX WPI; 1999-303011/25.
 XX
 XX New nucleic acid cloning methods.
 PT
 XX Disclosure; Page 170; 185pp; English.
 XX
 XX The invention relates to novel methods for cloning or subcloning one or
 CC more nucleic acid molecules (NAs) comprising: (a) combining in vitro or
 CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
 CC more desired nucleic acid segments flanked by at least 2 recombination
 CC sites which do not recombine with each other; (2) one or more vector
 CC donor molecules (VDMs) comprising at least 2 recombination sites which
 CC do not recombine with each other; and (3) one or more site-specific
 CC recombination proteins; (b) incubating the combination to transfer one or
 CC more of the desired segments into one or more of the VDMs, thereby
 CC producing one or more desired product molecules (PMs). The methods can be
 CC used for the efficient and specific recombination of NAM segments. They
 CC can be used to generate chimeric DNA or RNA molecules that have the
 CC desired characteristics and/or nucleic acid segments. The methods can
 CC also be used for changing vectors. The oligonucleotides AAX78935-X78994
 CC are used in the method of the invention
 XX
 XX Sequence 25 BP; 4 A; 3 C; 3 G; 9 T; 0 U; 6 Other;
 SQ
 Query Match 84.8%; Score 21.2; DB 2; Length 25;
 Best Local Similarity 76.0%; Pred. No. 2.1;
 Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GTTCAGCTTCTCKTRTACNAACTSGB 25
 |||||||
 Db 1 GTTCAGCTTCTCKTRTACNAACTSGB 25
 |||||||

RESULT 15
 AAT48219
 ID AAT48219 standard; DNA; 25 BP.
 XX
 AC AAT48219;
 XX
 DT 20-OCT-1997 (first entry)
 XX
 DE attR2 core region.
 XX
 KW att recombination site; core region; mutation; enhance; recombination;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:19 ; Search time 35.9 Seconds
(without alignments)
494.978 Million cell updates/sec

Title: US-10-820-133-3

Perfect score: 25

Sequence: 1 gttcagtttcttactnaactsgb 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	88.0	25	3	US-09-233-493-3
2	22	88.0	25	3	US-09-005-476-3
3	22	88.0	25	3	US-09-233-492-3
4	22	88.0	25	3	US-09-296-280-3
5	22	88.0	25	4	US-09-498-074-3
6	22	88.0	25	4	US-09-498-074-3
7	22	88.0	25	5	PCT-US96-10082A-3
8	21.2	84.8	25	3	US-09-296-280-42
9	20.8	83.2	25	3	US-09-233-493-10
10	20.8	83.2	25	3	US-09-005-476-10
11	20.8	83.2	25	3	US-09-233-492-10
12	20.8	83.2	25	3	US-09-296-280-10
13	20.8	83.2	25	4	US-09-498-074-10
14	20.8	83.2	25	4	US-09-498-074-10
15	20.8	83.2	25	5	PCT-US96-10082A-10
16	20.4	81.6	25	3	US-09-296-280-11
17	20	80.0	25	3	US-09-233-493-5
18	20	80.0	25	3	US-09-005-476-5
19	20	80.0	25	3	US-09-233-492-5
20	20	80.0	25	3	US-09-296-280-5
21	20	80.0	25	4	US-09-498-074-5
22	20	80.0	25	4	US-09-498-074-5
23	20	80.0	25	5	PCT-US96-10082A-5
24	19.6	78.4	25	3	US-09-233-493-1
25	19.6	78.4	25	3	US-09-005-476-1
26	19.6	78.4	25	3	US-09-233-492-1
27	19.6	78.4	25	3	US-09-296-280-1

28 19.6 78.4 25 4 US-09-498-074-1 Sequence 1, Appli
29 19.6 78.4 25 4 US-09-498-074-1 Sequence 1, Appli
30 19.6 78.4 25 5 PCT-US96-10082A-1 Sequence 1, Appli
31 19.2 76.8 25 3 US-09-233-493-9 Sequence 9, Appli
32 19.2 76.8 25 3 US-09-233-493-11 Sequence 11, Appli
33 19.2 76.8 25 3 US-09-233-493-16 Sequence 16, Appli
34 19.2 76.8 25 3 US-09-005-476-9 Sequence 9, Appli
35 19.2 76.8 25 3 US-09-005-476-11 Sequence 11, Appli
36 19.2 76.8 25 3 US-09-005-476-16 Sequence 16, Appli
37 19.2 76.8 25 3 US-09-233-492-9 Sequence 9, Appli
38 19.2 76.8 25 3 US-09-233-492-11 Sequence 11, Appli
39 19.2 76.8 25 3 US-09-233-492-16 Sequence 16, Appli
40 19.2 76.8 25 3 US-09-296-280-9 Sequence 9, Appli
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42 19.2 76.8 25 3 US-09-296-280-39 Sequence 39, Appli
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44 19.2 76.8 25 4 US-09-498-074-11 Sequence 11, Appli
45 19.2 76.8 25 4 US-09-498-074-16 Sequence 16, Appli

ALIGNMENTS

RESULT 1
US-09-233-493-3
; Sequence 3, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
US-09-233-493-3

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Query Match      88.0%; Score 22; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTCKTRTACNAACTSG 25
    |||||
Db 1 GTTCAGCTTCTCKTRTACNAACTSG 25

RESULT 2
US-09-005-476-3
; Sequence 3, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-3

Query Match      88.0%; Score 22; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTCKTRTACNAACTSG 25
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Db 1 GTTCAGCTTCTCKTRTACNAACTSG 25

RESULT 3
US-09-233-492-3
; Sequence 3, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2600
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-492-3

Query Match      88.0%; Score 22; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTCKTRTACNAACTSG 25
    |||||
Db 1 GTTCAGCTTCTCKTRTACNAACTSG 25

RESULT 4
US-09-296-280-3
; Sequence 3, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-3
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```
Query Match      88.0%; Score 22; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCKTRTACNAACTSGB 25
Db 1 GTTCAGCTTTCKTRTACNAACTSGB 25

RESULT 5
US-09-498-074-3
; Sequence 3, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: 04-Feb-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-498-074-3

Query Match      88.0%; Score 22; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCKTRTACNAACTSGB 25
Db 1 GTTCAGCTTTCKTRTACNAACTSGB 25

RESULT 6
US-09-498-074-3
; Sequence 3, Application US/09498074
; Patent No. 6720140
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: 04-Feb-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
US-09-498-074-3

Query Match      88.0%; Score 22; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCKTRTACNAACTSGB 25
Db 1 GTTCAGCTTTCKTRTACNAACTSGB 25

RESULT 7
PCT-US96-10082A-3
; Sequence 3, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: 04-Feb-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
US-09-498-074-3
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APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
RECOMBINATION SITES
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,074
FILING DATE: 04-Feb-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-498-074-3

Query Match      88.0%; Score 22; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCKTRTACNAACTSGB 25
Db 1 GTTCAGCTTTCKTRTACNAACTSGB 25

RESULT 7
PCT-US96-10082A-3
; Sequence 3, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: 04-Feb-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
US-09-498-074-3
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APPLICATION NUMBER: US/09/005,476
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
US-09-005-476-10

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 0.28;
Matches 20; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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|||||:|||||:|||||:|||||:
Db 1 GTTCAGCTTCTTGTACAAACTTGT 25

RESULT 11
US-09-233-492-10
Sequence 10, Application US/09233492
Patent No. 6270969
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
US-09-233-492-10

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 0.28;
Matches 20; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Db 1 GTTCAGCTTCTTGTACAAACTTGT 25

RESULT 12
US-09-296-280-10
Sequence 10, Application US/09296280
Patent No. 6277608
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary P.
APPLICANT: Fox, Donna K.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850007
CURRENT APPLICATION NUMBER: US/09/296,280
CURRENT FILING DATE: 1999-04-22
EARLIER APPLICATION NUMBER: US 09/177,387
EARLIER FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: US 60/065,930
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 25
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: recombination
OTHER INFORMATION: products
US-09-296-280-10

Query Match 83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 0.28;
Matches 20; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Db 1 GTTCAGCTTCTTGTACAAACTTGT 25

RESULT 13
US-09-498-074-10
Sequence 10, Application US/09498074
Patent No. 6534264
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,074
FILING DATE: (Herewith)
CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
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; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-498-074-10

Query Match      83.2%; Score 20.8; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 0.28;
Matches 20; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Db 1 GTTCAGCTTTCTGTACAACTTGT 25

RESULT 14
US-09-498-074-10
; Sequence 10, Application US/09498074
; Patent No. 6720140
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
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; FILING DATE: 04-Feb-2000
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; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
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; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
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; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
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US-09-498-074-10

Query Match      83.2%; Score 20.8; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 0.28;
Matches 20; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Db 1 GTTCAGCTTTCTGTACAACTTGT 25

RESULT 15
PCT-US96-10082A-10
; Sequence 10, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; RECOMBINATION SITES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
PCT-US96-10082A-10

Query Match      83.2%; Score 20.8; DB 5; Length 25;
Best Local Similarity 80.0%; Pred. No. 0.28;
Matches 20; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Db 1 GTTCAGCTTTCTGTACAACTTGT 25

Search completed: November 16, 2004, 10:22:30
Job time : 35.9 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:34:49 ; Search time 314 Seconds
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Title: US-10-820-133-3

Perfect score: 25

Sequence: 1 gtcagcttcttctacnaactsgb 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	22	88.0	25	9	US-09-822-634-4
3	22	88.0	25	9	US-09-907-900-3
4	22	88.0	25	9	US-09-907-719-3
5	22	88.0	25	10	US-09-432-085-3
6	22	88.0	25	10	US-09-985-448-3
7	22	88.0	25	14	US-10-058-292-3
8	22	88.0	25	14	US-10-058-291-3
9	22	88.0	25	14	US-10-162-879-3
10	22	88.0	25	15	US-10-161-403-43
11	22	88.0	25	15	US-10-300-892-3
12	22	88.0	25	16	US-10-680-316-3

13	22	88.0	25	17	US-10-815-730-3	Sequence 3, Appli
14	22	88.0	25	17	US-10-820-133-3	Sequence 3, Appli
15	22	88.0	25	18	US-10-161-408-35	Sequence 35, Appli
16	22	88.0	25	18	US-10-796-868A-3	Sequence 3, Appli
17	21.2	84.8	25	9	US-09-855-797A-42	Sequence 42, Appli
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36	20.8	83.2	25	16	US-10-680-316-10	Sequence 10, Appli
37	20.8	83.2	25	17	US-10-815-730-10	Sequence 10, Appli
38	20.8	83.2	25	17	US-10-820-133-10	Sequence 10, Appli
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40	20.8	83.2	25	18	US-10-796-868A-10	Sequence 10, Appli
41	20.8	83.2	43	9	US-09-732-914-45	Sequence 45, Appli
42	20.4	81.6	25	9	US-09-732-914-12	Sequence 12, Appli
43	20.4	81.6	25	9	US-09-855-797A-11	Sequence 11, Appli
44	20.4	81.6	25	9	US-09-907-900-11	Sequence 11, Appli
45	20.4	81.6	25	9	US-09-907-719-11	Sequence 11, Appli

ALIGNMENTS

RESULT 1

US-09-855-797A-3

; Sequence 3, Application US/09855797A

; Patent No. US20020094574A1

; GENERAL INFORMATION:

; APPLICANT: Hartley, James L.

; APPLICANT: Brasch, Michael A.

; APPLICANT: Temple, Gary F.

; APPLICANT: Fox, Donna K.

; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having

; TITLE OF INVENTION: Recombination Sites

; FILE REFERENCE: 0942.2850008

; CURRENT APPLICATION NUMBER: US/09/855.797A

; CURRENT FILING DATE: 2001-05-16

; PRIOR APPLICATION NUMBER: 09/296,281

; PRIOR FILING DATE: 1999-04-22

; PRIOR APPLICATION NUMBER: US 60/065,930

; PRIOR FILING DATE: 1997-10-24

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Unknown

; FEATURE:

; NAME/KEY: OTHER

; LOCATION: 18

; OTHER INFORMATION: "n" may be any nucleotide

; OTHER INFORMATION: Description of Unknown Organism: recombination

; OTHER INFORMATION: products

US-09-855-797A-3

Query Match 88.0%; Score 22; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTTCAGCTTTCKTRTACNAACTSGB 25

RESULT 2

US-09-822-634-4
; Sequence 4, Application US/09822634
; Patent No. US20020150556A1
; GENERAL INFORMATION:
; APPLICANT: Vile, Richard G.
; APPLICANT: Harrington, Kevin
; APPLICANT: Bateman, Andrew
; APPLICANT: Murphy, Steven
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TISSUE
; TITLE OF INVENTION: SPECIFIC GENE REGULATION THERAPY
; FILE REFERENCE: 07039-289001
; CURRENT APPLICATION NUMBER: US/09/822,634
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/193,977
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated vector sequence
; NAME/KEY: misc.feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: n = A,T,C or G
US-09-822-634-4

Query Match 88.0%; Score 22; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCKTRTACNAACTSGB 25
|||||
Db 1 GTTCAGCTTTCKTRTACNAACTSGB 25

RESULT 3

US-09-907-900-3
; Sequence 3, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.285004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-3

Query Match 88.0%; Score 22; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCKTRTACNAACTSGB 25
|||||
Db 1 GTTCAGCTTTCKTRTACNAACTSGB 25

RESULT 4

US-09-907-719-3
; Sequence 3, Application US/09907719
; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.285004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-719-3

Query Match 88.0%; Score 22; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTCKTRTACNAACTSGB 25
|||||
Db 1 GTTCAGCTTTCKTRTACNAACTSGB 25

RESULT 5

US-09-432-085-3
; Sequence 3, Application US/09432085
; Publication No. US20030100110A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085

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; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-432-085-3

Query Match 88.0%; Score 22; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTTCAGCTTCTKTRTACNAACTSGB 25
Db 1 GTTCAGCTTCTKTRTACNAACTSGB 25

RESULT 6
US-09-985-448-3
; Sequence 3, Application US/09985448
; Publication No. US20030157716A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.285004
; CURRENT APPLICATION NUMBER: US/09/985,448
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-985-448-3

Query Match 88.0%; Score 22; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTTCAGCTTCTKTRTACNAACTSGB 25
Db 1 GTTCAGCTTCTKTRTACNAACTSGB 25

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTTCAGCTTCTKTRTACNAACTSGB 25
Db 1 GTTCAGCTTCTKTRTACNAACTSGB 25

RESULT 7
US-10-058-292-3
; Sequence 3, Application US/10058292
; Publication No. US2003005452A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/058,292
; FILING DATE: 30-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/432,085
; FILING DATE: 1999-11-02
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-058-292-3

Query Match 88.0%; Score 22; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTTCAGCTTCTKTRTACNAACTSGB 25
Db 1 GTTCAGCTTCTKTRTACNAACTSGB 25

RESULT 8
US-10-058-291-3
; Sequence 3, Application US/10058291
; Publication No. US20030064515A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
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/
/ TITLE OF INVENTION: Recombinational Cloning Using Engineered
/ Recombination Sites
/
/ NUMBER OF SEQUENCES: 35
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
/ STREET: 1100 New York Ave., N. W. Suite 600
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3934
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
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/ CURRENT APPLICATION DATA: US/10/058,291
/ APPLICATION NUMBER: 09/432,085
/ FILING DATE: 1999-11-02
/ APPLICATION NUMBER: 09/233,493
/ FILING DATE: 20-JAN-1999
/ APPLICATION NUMBER: 09/005,476
/ FILING DATE: 12-JAN-1998
/ APPLICATION NUMBER: 08/663,002
/ FILING DATE: 07-JUN-1996
/ APPLICATION NUMBER: 08/486,139
/ FILING DATE: 07-JUN-1995
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: both
/ MOLECULE TYPE: cdna
/ SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-058-291-3

Query Match 88.0%; Score 22; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTKTRTACNAACTSG 25
Db 1 GTTCAGCTTCTKTRTACNAACTSG 25

RESULT 9
US-10-162-879-3
; Sequence 3, Application US/10162879
; Publication No. US20030068799A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
/
/ TITLE OF INVENTION: Recombinational Cloning Using Engineered
/ Recombination Sites
/
/ NUMBER OF SEQUENCES: 35
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
/ STREET: 1100 New York Ave., N. W. Suite 600
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3934
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
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/ SOFTWARE: PatentIn Release #1.0, Version #1.30
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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/162,879
/ FILING DATE: 06-Jun-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/432,085
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: 09/233,493
/ FILING DATE: 20-JAN-1999
/ APPLICATION NUMBER: 09/005,476
/ FILING DATE: 12-JAN-1998
/ APPLICATION NUMBER: 08/663,002
/ FILING DATE: 07-JUN-1996
/ APPLICATION NUMBER: 08/486,139
/ FILING DATE: 07-JUN-1995
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: both
/ MOLECULE TYPE: cdna
/ SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-162-879-3

Query Match 88.0%; Score 22; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTCTKTRTACNAACTSG 25
Db 1 GTTCAGCTTCTKTRTACNAACTSG 25

RESULT 10
US-10-161-403-43
; Sequence 43, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
/
/ TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
/ FILE REFERENCE: 24601-420
/ CURRENT APPLICATION NUMBER: US/10/161,403
/ CURRENT FILING DATE: 2002-05-30
/ PRIOR APPLICATION NUMBER: 60/294,758
/ PRIOR FILING DATE: 2001-05-30
/ PRIOR APPLICATION NUMBER: 60/366,891
/ PRIOR FILING DATE: 2002-03-21
/ NUMBER OF SEQ ID NOS: 129
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 43
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: m-attr
/ NAME/KEY: misc_difference
/ LOCATION: 18
/ OTHER INFORMATION: n is a o r g o r c o r t/u
US-10-161-403-43
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Query Match 88.0%; Score 22; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTKTRTACNAACTSGB 25
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Db 1 GTTCAGCTTTCTKTRTACNAACTSGB 25

RESULT 11

US-10-300-892-3
; Sequence 3, Application US/10300892
; Publication No. US20030175970A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/300,892
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-10-300-892-3

Query Match 88.0%; Score 22; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTKTRTACNAACTSGB 25
|||||
Db 1 GTTCAGCTTTCTKTRTACNAACTSGB 25

RESULT 12

US-10-680-316-3
; Sequence 3, Application US/10680316
; Publication No. US20040063207A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/680,316
; CURRENT FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: US/09/177,387A
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 25

; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-10-680-316-3

Query Match 88.0%; Score 22; DB 16; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTKTRTACNAACTSGB 25
|||||
Db 1 GTTCAGCTTTCTKTRTACNAACTSGB 25

RESULT 13

US-10-815-730-3
; Sequence 3, Application US/10815730
; Publication No. US20040171156A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/815,730
; CURRENT FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US/09/177,387A
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-10-815-730-3

Query Match 88.0%; Score 22; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTKTRTACNAACTSGB 25
|||||
Db 1 GTTCAGCTTTCTKTRTACNAACTSGB 25

RESULT 14

US-10-820-133-3
; Sequence 3, Application US/10820133
; Publication No. US20040171157A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/820,133
; CURRENT FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: US/09/177,387A
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 25

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; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/820,133
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US/09/177,387A
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-10-820-133-3

Query Match      88.0%; Score 22; DB 17; Length 25;
Best Local Similarity 100.0%; Pred.No. 0.58;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTTCAGCTTCKTRTACNAACTSGB 25
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Db       1 GTTCAGCTTCKTRTACNAACTSGB 25

RESULT 15
US-10-161-408-35
; Sequence 35, Application US/10161408
; Publication No. US20040214290A1
; GENERAL INFORMATION:
; APPLICANT: Perez, Carl
; APPLICANT: Fabijanski, Steven
; APPLICANT: Perkins, Edward
; TITLE OF INVENTION: Plant Artificial Chromosomes, Uses thereof, and Methods of Preparation
; TITLE OF INVENTION: Plant Artificial Chromosomes
; FILE REFERENCE: 24601-419
; CURRENT APPLICATION NUMBER: US/10/161,408
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: US 60/294,687
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: US 60/296,329
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: m-atrr recognition sequence
; FEATURE:
; NAME/KEY: misc_difference
; LOCATION: 18
; OTHER INFORMATION: n is a or g or c or t/u
US-10-161-408-35

Query Match      88.0%; Score 22; DB 18; Length 25;
Best Local Similarity 100.0%; Pred.No. 0.58;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTTCAGCTTCKTRTACNAACTSGB 25
        |||||
Db       1 GTTCAGCTTCKTRTACNAACTSGB 25

Search completed: November 16, 2004, 11:14:58
Job time : 314.1 secs
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:04 ; Search time 1532 Seconds
(without alignment)
594.643 Million cell updates/sec

Title: US-10-820-133-3

Perfect score: 25
Sequence: 1 gttcagtttcttactnaactsgb 25

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_ges1:*
9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	20.2	80.8	708	8	AQ990869 Rfc01706
C 2	20	80.0	829	9	CC863243 ND.L.10401
C 3	20	80.0	836	8	CC118013 ND.L.78N18
C 4	19	76.0	770	8	AQ991774 Rfc02039F
C 5	19	76.0	791	8	AQ991791 Rfc02368F
C 6	19	76.0	1161	7	CK162252 FGAS01484
C 7	18.8	75.2	321	2	BF086649 CM0-GN007
C 8	18.8	75.2	595	2	AW993039 RC2-BN003
C 9	18.8	75.2	635	7	CN484020 hw41b03.Y
C 10	18.8	75.2	672	8	AQ990864 Rfc01701
C 11	18.8	75.2	706	4	B1836912 603084230
C 12	18.8	75.2	714	5	BX359053 BX359053
C 13	18.8	75.2	752	4	BG620766 602617479
C 14	18.8	75.2	753	8	AQ990861 Rfc01698
C 15	18.8	75.2	797	4	BG427603 602497040
C 16	18.8	75.2	805	7	CR629462 DKFZp493K
C 17	18.8	75.2	808	8	AQ990388 Rfc01153
C 18	18.8	75.2	810	5	BQ216337 AGENCOURT
C 19	18.8	75.2	824	4	BG620383 602617507
C 20	18.8	75.2	831	5	BQ230007 AGENCOURT
C 21	18.8	75.2	852	4	BG401996 602466712
C 22	18.8	75.2	855	2	BE785867 601478671
C 23	18.8	75.2	856	2	BE893159 601437059
C 24	18.8	75.2	859	5	BX398237 BX398237

25	18.8	75.2	862	2	BE895530
26	18.8	75.2	908	4	BI546971 603190186
27	18.8	75.2	954	5	BQ893686 AGENCOURT
28	18.8	75.2	986	5	BX398580 BX398580
29	18.8	75.2	994	4	BM804936 AGENCOURT
30	18.8	75.2	1019	2	BE300319 600944384
31	18.4	73.6	94	7	CF652584 64-L02052
32	18.4	73.6	95	7	CF652701 71-L02052
33	18.4	73.6	127	9	CL308706 03S0467-1
C 34	18.4	73.6	628	6	CD324539 StrFu537.
C 35	18.2	72.8	402	9	CL604547 CH240_180
C 36	18.2	72.8	444	9	AG239085 Lotus cor
C 37	18.2	72.8	509	8	AQ165422 HS_3031.A
C 38	18.2	72.8	794	8	BM092933 RPi-24-3
C 39	18.2	72.8	1000	5	BU60343 603501901
C 40	18.2	72.8	1770	9	AG081618 Pan trogl
C 41	18	72.0	613	8	AZ431189 IM0216C04
C 42	18	72.0	686	4	BJ606288 BJ606288
C 43	18	72.0	707	4	BJ588203 BJ588203
C 44	18	72.0	756	8	AQ991732 Rfc00380F
C 45	18	72.0	762	4	BJ611386 BJ611386

ALIGNMENTS

RESULT 1
AQ990869/c
LOCUS
DEFINITION
708 bp DNA linear GSS 14-AUG-2000
Rfc01706 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01706, genomic survey
sequence.
ACCESSION
AQ990869
VERSION
AQ990869.1 GI:9649463
KEYWORDS
GSS.
SOURCE
Photorhabdus luminescens
ORGANISM
Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE
1 (bases 1 to 708)
ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
20378633
PUBMED
10919786
COMMENT
Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsarf@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to B.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: Shotgun.
Location/Qualifiers
1. .708
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG01706"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

FEATURES source

ORIGIN

```
Query Match      80.8%; Score 20.2; DB 8; Length 708;
Best Local Similarity 79.2%; Pred. No. 48;
Matches 19; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

[illegible]

Department of Eukaryotic Genomics
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
Library was provided by David Severson
Seq primer: SP6
Class: BAC ends.

```

FEATURES
  source
    Class: LNC ends.
    Location/Qualifiers
      1..829
        /organism="Aedes aegypti"
        /mol_type="genomic DNA"
        /strain="Liverpool"
        /db_xref="taxon:7159"
        /clone="NotreDame Liverpool-104015"
        /clone_lib="Notre Dame Liverpool"
        /note="Vector: pEGAC1; Site 1: Hind III; The library was
        prepared from whole body tissue of newly hatched L1 larvae
        by David Severison at the University of Notre Dame and
        Hongbin Zhang"

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Query Match	80.0%	Score 20;	DB 9;	Length 829;
Best Local Similarity	78.3%	Pred. No. 62;		
Matches	18;	Conservative	4;	Mismatches 1;
Indels	0;	Gaps	0;	
QY	3	TCAGCTTCTKTRTACNAACTSG	25	
Db	382	TCAGCTTTCGTATACCAACTCGT	404	

RESULT 3	CC118013	NDL.78N18.17	Notre Dame Liverpool	836 bp	DNA	linear	GSS 16-APR-2003
LOCUS	CC118013	NDL.78N18.17	Notre Dame Liverpool	836 bp	DNA	linear	GSS 16-APR-2003
DEFINITION	CC118013	NDL.78N18.17	Notre Dame Liverpool	836 bp	DNA	linear	GSS 16-APR-2003
ACCESSION	CC118013	NDL.78N18.17	Notre Dame Liverpool	836 bp	DNA	linear	GSS 16-APR-2003
VERSION	CC118013.1	NDL.78N18.17	Notre Dame Liverpool	836 bp	DNA	linear	GSS 16-APR-2003
KEYWORDS	GSS.	NDL.78N18.17	Notre Dame Liverpool	836 bp	DNA	linear	GSS 16-APR-2003
SOURCE	Aedes aegypti (yellow fever mosquito)	NDL.78N18.17	Notre Dame Liverpool	836 bp	DNA	linear	GSS 16-APR-2003
ORGANISM	Aedes aegypti	NDL.78N18.17	Notre Dame Liverpool	836 bp	DNA	linear	GSS 16-APR-2003
	Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;	NDL.78N18.17	Notre Dame Liverpool	836 bp	DNA	linear	GSS 16-APR-2003

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1
2
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100

Stegomyia.
1 (bases 1 to 836)
Lotus.B., Shetty,J., Knudson,D. and Severson,D.
BAC end sequencing of Aedes aegypti
Unpublished (2003)
Other GSSs: NDL.78N18.SP6
Contact: Brendan Loftus
Department of Eukaryotic Genomics
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
Library was provided by David Severson
Seq primer: 17
Class: BAC ends.

FEATURES	SOURCE
1. High Accuracy: The model achieves a high accuracy rate, consistently performing well across various datasets and tasks.	1. High Accuracy: The model achieves a high accuracy rate, consistently performing well across various datasets and tasks.
2. Scalability: The model is designed to handle large-scale data and complex tasks, making it suitable for enterprise-level applications.	2. Scalability: The model is designed to handle large-scale data and complex tasks, making it suitable for enterprise-level applications.
3. Interpretability: The model's decisions are transparent and explainable, allowing users to understand the underlying logic and reasoning.	3. Interpretability: The model's decisions are transparent and explainable, allowing users to understand the underlying logic and reasoning.
4. Robustness: The model is highly resistant to adversarial attacks and data poisoning, ensuring reliable performance in real-world scenarios.	4. Robustness: The model is highly resistant to adversarial attacks and data poisoning, ensuring reliable performance in real-world scenarios.
5. Efficiency: The model is optimized for fast inference and low resource consumption, making it ideal for deployment on edge devices.	5. Efficiency: The model is optimized for fast inference and low resource consumption, making it ideal for deployment on edge devices.

```
1..836
/organism="Aedes aegypti"
/mol_type="genomic DNA"
/strain="liverpool"
/db_xref="taxon:7159"
/clone="NDL.78N18"
/clone_lib="Notre Dame Li
/notes="Vector: pECBAC1; S
prepared from whole body
by David Severson at the
Hongbin Zhang"
```

ORIGIN

```
Query Match      80.0%; Score 20; DB 8; Length 836;
Best Local Similarity 78.3%; Pred. No. 62;
Matches 18; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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RESULT 4
AO991774/C

LOCUS	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
AQ991774	AQ991774	AQ991774	GSS.	Photobabduus luminescens	Photobabduus luminescens
DEFINITION					
LOCUS	AQ991774	770 bp	DNA	linear	GSS 14-AUG-2000
DEFINITION	RFC02039F	Photobabduus luminescens strain W14 M13 library			
LOCUS	AQ991774	770 bp	DNA	linear	GSS 14-AUG-2000
DEFINITION	RFC02039F	Photobabduus luminescens genomic clone PUG02039F, genomic survey sequence.			
ACCESSION	AQ991774	AQ991774	GI:9650368		
VERSION	AQ991774	AQ991774			
KEYWORDS			GSS.		
SOURCE				Photobabduus luminescens	Photobabduus luminescens
ORGANISM					

REFERENCE
AUTHORS

TITLE
A genomic sample sequence of the entomopathogenic bacterium
Photobacterium luminescens W14: potential implications for virulence

JOURNAL
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

MEDLINE
20378633

PUBMED
10919786

CONTACT: Dr. Michael Constantine
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826671
Tel: (44) 1225 826672
Fax: (44) 1225 826679
Email: bsarfc@bath.ac.uk
This is one of a selected subset of full
library. For annotation of identified
mapping to E. coli K12 genome) please
2000, Nucleic Acids Res.
Seq primer: M13 Reverse
Class: shotgun.

```

FEATURES
  source
    Location/Qualifiers
      1..770
        /organism="Photorhabdus luminescens"
        /mol_type="genomic DNA"
        /strain="W14"
        /db_xref="taxon:29488"
        /clones="PLG02039F"
        /dev_stages="primary phase variant"
        /clone_libs="Photorhabdus luminescens strain W14 M13 library"
        /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN
  Query Match          76.0%; Score 19; DB 8; Length 770;
  Best Local Similarity 79.2%; Pred. No. 2e+02;
  Matches 19; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCKTRTACNAACTSG 24
    ||||| :|||
Db 59 GTTCAGCTTTTATACTACTG 36
    ||||| :|||

RESULT 5
AQ991791/c
LOCUS
DEFINITION
  AQ991791 791 bp DNA linear GSS 14-AUG-2000
  Rf02368F Photorhabdus luminescens strain W14 M13 library
  Photorhabdus luminescens genomic clone PLG02368F, genomic survey
  sequence.
ACCESSION
  AQ991791
VERSION
  AQ991791.1 GI:9650385
KEYWORDS
  GSS.
SOURCE
  Photorhabdus luminescens
  ORGANISM
    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
    Enterobacteriaceae; Photorhabdus.
REFERENCE
  1 (bases 1 to 791)
  Daborn,P.J., Bowen,D. and Blattner,F.R.
  A genomic sample sequence of the entomopathogenic bacterium
  Photorhabdus luminescens W14: potential implications for virulence
  Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
JOURNAL
  MEDLINE
  PUBMED
  10919786
COMMENT
  Contact: ffrench-Constant RH
  Department of Biology and Biochemistry
  University of Bath
  South Building, Bath BA2 7AY, UK
  Tel: (44) 1225 826621
  Fax: (44) 1225 826779
  Email: bsarfc@bath.ac.uk
  This is one of a selected subset of flipped clones from the M13
  library. For annotation of identified clones (BLASTX, BLASTN and
  mapping to E. coli K12 genome) please see ffrench-Constant et al.
  2000, Nucleic Acids Res.
  Seq primer: M13 Reverse
  Class: shotgun.
FEATURES
  source
    Location/Qualifiers
      1..791
        /organism="Photorhabdus luminescens"
        /mol_type="genomic DNA"
        /strain="W14"
        /db_xref="taxon:29488"
        /clones="PLG02368F"
        /dev_stages="primary phase variant"
        /clone_libs="Photorhabdus luminescens strain W14 M13 library"
        /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN
  Query Match          76.0%; Score 19; DB 8; Length 791;
  Best Local Similarity 79.2%; Pred. No. 2e+02;

FEATURES
  source
    Location/Qualifiers
      1..1161
        /organism="Triticum aestivum"
        /mol_type="mRNA"
        /db_xref="taxon:4565"
        /clone_lib="Triticum aestivum FGAS: Library 4 Gate 8"
        /note="Organ: Crown and leaf; Vector: pCMV.SPORI6;
        Conditions for growth: Seeds were germinated in a
        water-saturated mix (50% black earth and 50% ProMix) in a
        growth chamber for 7 days under an irradiance of 200 mmol
        m-2 sec-1. The temperature was maintained at 20 degrees C
        with a 15-hr photoperiod under a relative humidity of 70%.
        After this period watering of plants was stopped. Four
        time points were sampled during a two week period; the
        first after wilting was observed and the last, two weeks
        later, consisted of live crown and leaf tissue (leaf
        tissue that was yellow was not included in sampled
        material). First strand synthesis in this library was done
        in the presence of methylated dCTP thereby protecting from
        internal cleavage with NotI."

ORIGIN
  Query Match          76.0%; Score 19; DB 7; Length 1161;
  Best Local Similarity 77.3%; Pred. No. 2.le+02;
  Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAGCTTTCKTRTACNAACTSGB 25
    ||||| :|||
Db 553 CAGCTTTCTGTACAACTGGT 574
    ||||| :|||

RESULT 7

```

BF086649/c	BF086649	321 bp	linear	EST 19-OCT-2000
LOCUS	CM0-GN0077-160900-559-g06	GN0077	Homo sapiens	CDNA, mRNA sequence.
DEFINITION	BF086649			
ACCESSION	BF086649.1	GI:10892268		
VERSION				
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			

REFERENCE
AUTHORS

1 (bases 1 to 595)
Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

TITLE	JOURNAL	MEDLINE	PUBMED	COMMENT
1. <i>Journal of the American Medical Association</i>				
2. <i>British Medical Journal</i>				
3. <i>New England Journal of Medicine</i>				
4. <i>Lancet</i>				
5. <i>Annals of Internal Medicine</i>				
6. <i>Journal of Clinical Investigation</i>				
7. <i>Journal of Biological Chemistry</i>				
8. <i>Journal of the American Chemical Society</i>				
9. <i>Journal of the American Pharmaceutical Association</i>				
10. <i>Journal of the American Dietetic Association</i>				
11. <i>Journal of the American Nurses Association</i>				
12. <i>Journal of the American Physical Therapy Association</i>				
13. <i>Journal of the American Speech-Language-Hearing Association</i>				
14. <i>Journal of the American Psychological Association</i>				
15. <i>Journal of the American Psychiatric Association</i>				
16. <i>Journal of the American Geriatrics Society</i>				
17. <i>Journal of the American Geriatrics Society</i>				
18. <i>Journal of the American Geriatrics Society</i>				
19. <i>Journal of the American Geriatrics Society</i>				
20. <i>Journal of the American Geriatrics Society</i>				

FEATURES source

high quality sequences (99.2% identity).
Location/Qualifiers
1..595
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BN0033"
/note="Organ: breast normal; Vector: puc18; Site 1: Sma1;
Site 2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

```

Query Match      75.2%; Score 18.8; DB 2; Length 595;
Best Local Similarity 72.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GTTCAGCTTTCKTRTACNAACTSGB 25
        ||||| ||||| :||| ||| :|:
Db      88 GTTCTGCTTTCTTATACCAAGTGC 112

```

```

Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 41 row: b column: 03
Seq primer: M13RP1 reverse primer (ABI)
Location/Qualifiers
1. 635
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="hw41b03"
/cell_type="pericytes"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human primary human ocular pericytes.
Unamplified (hw)"
/note="Organ: Eye; Vector: pSPORT1; RNA was extracted from
primary human pericytes in culture. A directionally cloned
cDNA library in the pSPORT1 vector (Invitrogen) was
constructed at Bioserve Biotechnology (Laurel MD)
essentially following the protocols of the SuperScript
Plasmid System full details of which are contained in the
manufacturer's instruction manual
(http://www.lifetech.com/). First strand synthesis was
carried out using a Not I primer-adaptor
[5'-pGACTAGTTCTAGATCGAGCGGCCGCC(T)15-3']. cDNA was
cloned in Not I/Sal I sites. EST analysis was performed at
the NIH Intramural Sequencing Center (NISC)."
```

ORIGIN

Query Match 75.2%; Score 18.8; DB 7; Length 635;
Best Local Similarity 72.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTCTACNAACTSGB 25
|||||:|||||:|||||:|||||:|||||:
Db 637 GTTCAGCTTCTTATACCACTGSC 426

RESULT 10
AQ990864/c
LOCUS
DEFINITION Rf01701 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01701, genomic survey
sequence.
ACCESSION AQ990864
VERSION AQ990864.1 GI:9649458
KEYWORDS GSS.
SOURCE Photorhabdus luminescens
ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE 1 (bases 1 to 672)
AUTHORS ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
TITLE A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
MEDLINE 20378633
PUBMED 10319786
COMMENT Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsr1c@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.

FEATURES
source
Location/Qualifiers
1. 672
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG01701"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

ORIGIN

Query Match 75.2%; Score 18.8; DB 8; Length 672;
Best Local Similarity 72.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTCTACNAACTSGB 25
|||||:|||||:|||||:|||||:|||||:
Db 637 GTTCAGCTTCTTATACCACTGSC 613

RESULT 11
BI836912
LOCUS
DEFINITION 603084230f1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5223318 5',
mRNA sequence.
ACCESSION BI836912
VERSION BI836912.1 GI:15948462
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 706)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM1561 row: 1 column: 07
High quality sequence stop: 646.
Location/Qualifiers
1. 706
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5223318"
/lab_host="DH10B"
/clone_lib="NIH_MGC_120"
/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dr primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 75.2%; Score 18.8; DB 4; Length 706;
Best Local Similarity 72.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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Qy 1 GTTCAGCTTCTKTRTACNAACTSGB 25
    ||||| ||||| ||||| ||||| |||||
Db 269 GTTCTGCTTCTTATACCAAGTGGC 293

RESULT 12
LOCUS BX359053 714 bp mRNA linear EST 08-APR-2004
DEFINITION BX359053 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1052YG13 5-PRIME, mRNA sequence.
ACCESSION BX359053
VERSION BX359053.2 GI:46291338
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 714)
AUTHORS Li.W.B., Gruber.C., Jessee.J. and Polayes.D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 5, 2003 this sequence version replaced gi:30372318.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
470.1
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0D1052AD07QPI&c=470.r.
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/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6
vector. Library was normalized."

ORIGIN
Query Match 75.2%; Score 18.8; DB 5; Length 714;
Best Local Similarity 72.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTKTRTACNAACTSGB 25
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Db 548 GTTCTGCTTCTTATACCAAGTGGC 572

RESULT 13
BG620766 752 bp mRNA linear EST 18-APR-2001
LOCUS BG620766 752 bp mRNA linear EST 18-APR-2001
DEFINITION BG620766 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4731450 5',
mRNA sequence.
ACCESSION BG620766
VERSION BG620766.1 GI:13672137
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 752)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM1589 row: m column: 19
High quality sequence stop: 663.
FEATURES
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Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:4731450"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NIH_MGC_79"
/notes="Organ: placenta; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggcgctcgcc); Site 2: SfiI
(ggcattatggc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CAGGCGCATATGGCC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGCGGAGCGCGCATATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.3
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN
Query Match 75.2%; Score 18.8; DB 4; Length 752;
Best Local Similarity 72.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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Db 428 GTTCTGCTTCTTATACCAAGTGGC 452

RESULT 14
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LOCUS AQ990861/c 753 bp DNA linear GSS 14-AUG-2000
DEFINITION Rfc01698 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01698, genomic survey
sequence.
ACCESSION AQ990861
VERSION AQ990861.1 GI:9649455
KEYWORDS GSS.
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE 1 (bases 1 to 753)
AUTHORS ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattnr,F.R.
TITLE A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
JOURNAL 20378633
MEDLINE 10919786
PUBMED
COMMENT Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsarf@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.

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Best Local Similarity 72.0%; Pred: NO. 2.5e+02;
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Db 429 GTTCGCTTTCTTATACCAAGTGC 453

Search completed: November 16, 2004, 10:16:31
Job time : 1534 secs

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ORIGIN

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:29:43 ; Search time 708.5 Seconds
(without alignments)
1668.656 Million cell updates/sec

Title: US-10-820-133-4
Perfect score: 25
Sequence: 1 agccgcgcttttcktrtacnaaqtspb 25

Scoring table: IDENTITY_NUC
Gapop 10.0 ; Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

Database :
1: qb ba:*

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2: qb_hfq: *
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3: gb_III: *

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4: gb_oml: *
5: qb_oy: *
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5: gb_ov: *
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7: gb_ph: *
8: gb_sl: *
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[illegible]

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10: gb_ro:*
11: gb_ro:*
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11: gb_sts:
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12: gb_sy:*

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13: gb_un:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description	
1	21.6	86.4	25	6	AR124524	Sequence	
2	21.6	86.4	25	6	AR163175	Sequence	
3	21.6	86.4	25	6	AR493776	Sequence	
4	21.6	86.4	25	6	AX269134	Sequence	
5	21.6	86.4	25	6	AX491643	Sequence	
6	21.6	86.4	25	6	AX498614	Sequence	
7	21.6	86.4	25	6	BD131330	Recombina	
c	8	21.6	86.4	48	6	AX525436	Sequence
	9	20.4	81.6	25	6	AR124533	Sequence
	10	20.4	81.6	25	6	AR163184	Sequence
	11	20.4	81.6	25	6	AR493785	Sequence
12	20.4	81.6	25	6	AX269139	Sequence	
13	20.4	81.6	25	6	AX491652	Sequence	
14	20.4	81.6	25	6	AX498623	Sequence	
15	20.4	81.6	25	6	BD131339	Recombina	
16	20.4	81.6	25	6	BD131366	Recombina	
17	20.4	81.6	48	6	BD263257	Compositi	
18	20.4	81.6	48	6	BD263281	Compositi	
c	19	20.4	81.6	217173	10	AC122188	Mus muscu
	20	20.4	81.6	217173	10	AC122188	Mus muscu

ALIGNMENTS

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C 25	20	80.0	25	6	AX127349	Sequence
C 26	20	80.0	25	6	AX787488	Sequence
C 27	20	80.0	25	6	AX787510	Sequence
C 28	20	80.0	25	6	BD131334	Recombina
C 29	20	80.0	26	6	BD263242	Compositi
C 30	20	80.0	29	6	BD263254	Compositi
C 31	20	80.0	29	6	BD263275	Compositi
C 32	20	80.0	29	6	BD263315	Compositi
C 33	20	80.0	29	6	BD263322	Compositi
C 34	20	80.0	29	6	BD263326	Compositi
C 35	20	80.0	29	6	BD263331	Compositi
C 36	20	80.0	29	6	BD263337	Compositi
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C 39	20	80.0	29	6	AX787495	Sequence
C 40	20	80.0	29	6	BD161056	Method fo
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C 43	20	80.0	30	6	AX787489	Sequence
C 44	20	80.0	33	6	AX787490	Sequence
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ALIGNMENTS

RESULT 1

LOCUS

AR124524

SEQUENCE 4 from patent US 6171861.

AR124524

GI:14109885

Unknown.

Unknown.

Unclassified.

1 (bases 1 to 25)

Hartley,J.L. and Brasch,M.A.

Recombinational cloning using engineered recombination sites

Patent: US 6171861-A 4 09-JAN-2001;

Location/Qualifiers

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/organism="unknown"

/mol_type="unassigned DNA"

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

Query Match

Best Local Similarity

Matches

86.4%;

Score 21.6;

DB 6;

Length 25;

25;

Conservative

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Mismatches

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Indels

0;

Gaps

0;

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Db

1

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RESULT 2

LOCUS

AR163175

SEQUENCE 4 from patent US 6270969.

AR163175

GI:16233683

Unknown.

Unknown.

Unclassified.

1 (bases 1 to 25)

Hartley,J.L. and Brasch,M.A.

Recombinational cloning using engineered recombination sites

REFERENCE

AUTHORS

TITLE

JOURNAL Patent: US 6270969-A 4 07-AUG-2001;
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 Db 1 AGCCGCTTTCTKTRTACNAAGTSG 25

RESULT 3
 AR493776
 LOCUS 25 bp mRNA linear PAT 15-MAY-2004
 DEFINITION Sequence 4 from patent US 6720140.
 ACCESSION AR493776
 VERSION AR493776.1 GI:47266188
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 25)
 AUTHORS Hartley, J.L. and Brasch, M.A.
 TITLE Recombinational cloning using engineered recombination sites
 JOURNAL Patent: US 6720140-A 4 13-APR-2004;
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 DEFINITION Sequence 5 from Patent WO0174861.
 ACCESSION AX269134
 VERSION AX269134.1 GI:16542054
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1
 AUTHORS Ville, R.G., Harrington, K., Murphy, S. and Bateman, A.
 TITLE Compositions and methods for tissue specific gene regulation
 JOURNAL therapy
 Patent: WO 0174861-A 5 11-OCT-2001;
 MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
 FEATURES Location/Qualifiers
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 /note="Synthetically generated vector sequence"

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RESULT 5
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 LOCUS 25 bp DNA linear PAT 16-AUG-2002
 DEFINITION Sequence 4 from Patent EP1227147.
 ACCESSION AX491643
 VERSION AX491643.1 GI:22324151
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 REFERENCE 1
 AUTHORS Hartley, J.L. and Brasch, M.A.
 TITLE Recombinational cloning using engineered recombination sites
 JOURNAL Patent: EP 1227147-A 4 31-JUL-2002;
 INVITROGEN CORPORATION (US)
 FEATURES Location/Qualifiers
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ORIGIN

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 Db 1 AGCCGCTTTCTKTRTACNAAGTSG 25

RESULT 6
 AX498614
 LOCUS 25 bp DNA linear PAT 26-SEP-2002
 DEFINITION Sequence 4 from Patent EP1229113.
 ACCESSION AX498614
 VERSION AX498614.1 GI:23343411
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 REFERENCE 1
 AUTHORS Hartley, J.L. and Brasch, M.A.
 TITLE Recombinational cloning using engineered recombination sites
 JOURNAL Patent: EP 1229113-A 4 07-AUG-2002;
 INVITROGEN CORPORATION (US)
 FEATURES Location/Qualifiers
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 /db_xref="taxon:32644"

ORIGIN

Query Match 86.4%; Score 21.6; DB 6; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2.8;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCGCTTTCTKTRTACNAAGTSG 25
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 Db 1 AGCCGCTTTCTKTRTACNAAGTSG 25

RESULT 7
 BD131330
 LOCUS 25 bp DNA linear PAT 18-SEP-2002
 DEFINITION Recombinational cloning using nucleic acids having recombination sites.
 ACCESSION BD131330

<p>BD131330.1 GI:23226275</p> <p>JP 2002500861-A/4.</p> <p>unidentified</p> <p>unclassified</p> <p>REFERENCE 1 (bases 1 to 25)</p> <p>AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.</p> <p>TITLE Recombinational cloning using nucleic acids having recombination</p> <p>JOURNAL Patent: JP 2002500861-A 4 15-JAN-2002;</p> <p>COMMENT LIFE TECHNOLOGIES INC</p> <p>OS Unknown</p> <p>PN JP 2002500861-A/4</p> <p>PD 15-JAN-2002</p> <p>PR 26-OCT-1998 JP 2000518069</p> <p>PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI</p> <p>JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DONNA K FOX PC</p> <p>C12N15/09,C12Q1/68,C12N15/00</p> <p>CC Description of Unknown Organism: recombination products FH</p> <p>Key source Location/Qualifiers</p> <p>FT source 1..25</p> <p>FT Location/Qualifiers</p> <p>1..25</p> <p>/organism="unidentified"</p> <p>/mol_type="genomic DNA"</p> <p>/db_xref="taxon:32644"</p>	<p>Query Match 86.4%; Score 21.6; DB 6; Length 25;</p> <p>Best Local Similarity 100.0%; Pred.No.2.8;</p> <p>Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>	<p>Qy 1 AGCCWGCCTTCTKTRTACNAAGTSG 25</p> <p> : : : :</p> <p>Db 1 AGCCWGCCTTCTKTRTACNAAGTSG 25</p> <p> : : : :</p>	<p>RESULT 8</p> <p>AX525436/c</p> <p>LOCUS AX525436 48 bp DNA linear PAT 21-NOV-2002</p> <p>DEFINITION Sequence 34 from Patent WO02066622.</p> <p>ACCESSION AX525436</p> <p>VERSION AX525436.1 GI:25170322</p> <p>KEYWORDS synthetic construct</p> <p>SOURCE synthetic construct</p> <p>ORGANISM artificial sequences.</p> <p>REFERENCE 1</p> <p>AUTHORS Tautsami,N., Vind,J. and Patkar,S.A.</p> <p>TITLE Lipolytic enzyme genes</p> <p>JOURNAL Patent: WO 02066622-A 34 29-AUG-2002;</p> <p>Novozymes A/S (DK)</p> <p>FEATURES</p> <p>source</p> <p>1..48</p> <p>/organism="synthetic construct"</p> <p>/mol_type="unassigned DNA"</p> <p>/db_xref="taxon:32630"</p> <p>/note="051200J24"</p>	<p>Query Match 86.4%; Score 21.6; DB 6; Length 48;</p> <p>Best Local Similarity 76.0%; Pred.No.2.8;</p> <p>Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;</p>	<p>Qy 1 AGCCWGCCTTCTKTRTACNAAGTSG 25</p> <p> : : : :</p> <p>Db 29 AGCCAGCTTCTTGTTACAAAGTGGT 5</p> <p> : : : :</p>	<p>RESULT 9</p> <p>AR124533</p> <p>LOCUS AR124533 25 bp DNA linear PAT 16-MAY-2001</p> <p>DEFINITION Sequence 13 from patent US 6171861.</p>		
<p>AR124533</p> <p>AR124533.1 GI:14109894</p> <p>KEYWORDS</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unknown.</p> <p>REFERENCE 1 (bases 1 to 25)</p> <p>AUTHORS Hartley,J.L. and Brasch,M.A.</p> <p>TITLE Recombinational cloning using engineered recombination sites</p> <p>JOURNAL Patent: US 6171861-A 13 09-JAN-2001;</p> <p>FEATURES</p> <p>source</p> <p>1..25</p> <p>/organism="unknown"</p> <p>/mol_type="unassigned DNA"</p>	<p>Query Match 81.6%; Score 20.4; DB 6; Length 25;</p> <p>Best Local Similarity 76.0%; Pred.No.13;</p> <p>Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;</p>	<p>Qy 1 AGCCWGCCTTCTKTRTACNAAGTSG 25</p> <p> : : : :</p> <p>Db 1 AGCTGCTTCTTGTTACAAAGTTGG 25</p> <p> : : : :</p>	<p>RESULT 10</p> <p>AR163184</p> <p>LOCUS AR163184 25 bp DNA linear PAT 17-OCT-2000</p> <p>DEFINITION Sequence 13 from patent US 6270969.</p> <p>ACCESSION AR163184</p> <p>VERSION AR163184.1 GI:16233696</p> <p>KEYWORDS</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unknown.</p> <p>REFERENCE 1 (bases 1 to 25)</p> <p>AUTHORS Hartley,J.L. and Brasch,M.A.</p> <p>TITLE Recombinational cloning using engineered recombination sites</p> <p>JOURNAL Patent: US 6270969-A 13 07-AUG-2001;</p> <p>FEATURES</p> <p>source</p> <p>1..25</p> <p>/organism="unknown"</p> <p>/mol_type="unassigned DNA"</p>	<p>Query Match 81.6%; Score 20.4; DB 6; Length 25;</p> <p>Best Local Similarity 76.0%; Pred.No.13;</p> <p>Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;</p>	<p>Qy 1 AGCCWGCCTTCTKTRTACNAAGTSG 25</p> <p> : : : :</p> <p>Db 1 AGCTGCTTCTTGTTACAAAGTTGG 25</p> <p> : : : :</p>	<p>RESULT 11</p> <p>AR493785</p> <p>LOCUS AR493785 25 bp mRNA linear PAT 15-MAY-2000</p> <p>DEFINITION Sequence 13 from patent US 6720140.</p> <p>ACCESSION AR493785</p> <p>VERSION AR493785.1 GI:47266206</p> <p>KEYWORDS</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unknown.</p> <p>REFERENCE 1 (bases 1 to 25)</p> <p>AUTHORS Hartley,J.L. and Brasch,M.A.</p> <p>TITLE Recombinational cloning using engineered recombination sites</p> <p>JOURNAL Patent: US 6720140-A 13 13-APR-2004;</p> <p>FEATURES</p> <p>source</p> <p>1..25</p> <p>/organism="unknown"</p> <p>/mol_type="mRNA"</p>	<p>Query Match 81.6%; Score 20.4; DB 6; Length 25;</p> <p>Best Local Similarity 76.0%; Pred.No.13;</p> <p>Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;</p>	<p>Qy 1 AGCCWGCCTTCTKTRTACNAAGTSG 25</p> <p> : : : :</p> <p>Db 1 AGCTGCTTCTTGTTACAAAGTTGG 25</p> <p> : : : :</p>

Query Match 81.6%; Score 20.4; DB 6; Length 25;
Best Local Similarity 76.0%; Pred. No. 13;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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Db 1 AGCCTGCTTCTTGACAAAGTTGG 25

RESULT 12
AX269139
LOCUS AX269139 25 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 10 from Patent WO0174861.
ACCESSION AX269139
VERSION AX269139.1 GI:16542059
KEYWORDS .
ORGANISM synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Vile, R.G., Harrington, K., Murphy, S. and Bateman, A.
TITLE Compositions and methods for tissue specific gene regulation
therapy
JOURNAL Patent: WO 0174861-A 10 11-OCT-2001;
MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
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ORIGIN

Query Match 81.6%; Score 20.4; DB 6; Length 25;
Best Local Similarity 76.0%; Pred. No. 13;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCCGCTTCTCKTRTACNAAGTSG 25
||||:||||:||||:||||:||||:|
Db 1 AGCCTGCTTCTTGACAAAGTTGG 25

RESULT 13
AX491652
LOCUS AX491652 25 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 13 from Patent EP1227147.
ACCESSION AX491652
VERSION AX491652.1 GI:22324160
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE 1
AUTHORS Hartley, J.L. and Brasch, M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1227147-A 13 31-JUL-2002;
INVITROGEN CORPORATION (US)

FEATURES
source Location/Qualifiers
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 81.6%; Score 20.4; DB 6; Length 25;
Best Local Similarity 76.0%; Pred. No. 13;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCCGCTTCTCKTRTACNAAGTSG 25
||||:||||:||||:||||:||||:|
Db 1 AGCCTGCTTCTTGACAAAGTTGG 25

RESULT 14
AX498623
LOCUS AX498623 25 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 13 from Patent EP1229113.
ACCESSION AX498623
VERSION AX498623.1 GI:23343420
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE 1
AUTHORS Hartley, J.L. and Brasch, M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1229113-A 13 07-AUG-2002;
INVITROGEN CORPORATION (US)

FEATURES
source Location/Qualifiers
1..25
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 81.6%; Score 20.4; DB 6; Length 25;
Best Local Similarity 76.0%; Pred. No. 13;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCCGCTTCTCKTRTACNAAGTSG 25
||||:||||:||||:||||:||||:|
Db 1 AGCCTGCTTCTTGACAAAGTTGG 25

RESULT 15

BD131339
LOCUS BD131339 25 bp DNA linear PAT 18-SEP-2002
DEFINITION Recombinational cloning using nucleic acids having recombination sites.
ACCESSION BD131339
VERSION BD131339.1 GI:23226284
KEYWORDS JP 2002500861-A/13.
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley, J.L., Brasch, M.A., Temple, G.F. and Fox, D.K.
TITLE Recombinational cloning using nucleic acids having recombination sites.
JOURNAL Patent: JP 2002500861-A 13 15-JAN-2002;
LIFE TECHNOLOGIES INC

COMMENT OS Unknown
PN JP 2002500861-A/13
PD 15-JAN-2002
PF 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930, 23-OCT-1998 US 09/177387 PI
JAMES L. HARTLEY, MICHAEL A. BRASCH, GARY F. TEMPLE, DONNA K. FOX PC
C12N15/09, C12Q1/68, C12N15/00
CC Description of Unknown Organism: recombination products FH
Key Location/Qualifiers
FT source 1..25
FT /organism="Unknown".

FEATURES
source Location/Qualifiers
1..25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 81.6%; Score 20.4; DB 6; Length 25;
Best Local Similarity 76.0%; Pred. No. 13;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCCGCTTCTCKTRTACNAAGTSG 25
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Db 1 AGCCTGCTTCTTGACAAAGTTGG 25

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Job time : 709.5 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:29:13 ; Search time 167.8 Seconds
(without alignments)
782.095 Million cell updates/sec

Title: US-10-820-133-4

Perfect score: 25

Sequence: 1 agccwgtttcttctacnaagtsb 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 413486 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21.6	86.4	25	2	AAT48213
2	21.6	86.4	25	2	AAX78938
3	21.6	86.4	25	4	AAC87869
4	21.6	86.4	25	4	AAC87869 Escherich
5	21.6	86.4	25	4	Aaf55738
6	21.6	86.4	25	4	AAD14432
7	21.6	86.4	25	5	AAS14783
8	21.6	86.4	25	8	ABT16624
9	21.6	86.4	25	9	ACD28279
10	21.6	86.4	25	9	ADA38165
11	21.6	86.4	25	10	ACC44653
12	21.6	86.4	25	10	ACC44653
13	21.6	86.4	25	12	ADL93419
14	21.6	86.4	48	6	ABT12773
15	20.4	81.6	25	2	AAT48222
16	20.4	81.6	25	2	AAX78947
17	20.4	81.6	25	2	AAX78947 Oligonucl
18	20.4	81.6	25	4	AAC87878
19	20.4	81.6	25	4	Aaf55747
20	20.4	81.6	25	4	AAD14441
21	20.4	81.6	25	5	AAS14788

22	20.4	81.6	25	6	ABQ82125
23	20.4	81.6	25	8	ABT16632
24	20.4	81.6	25	9	ACD28288
25	20.4	81.6	25	9	ACD28488
26	20.4	81.6	25	9	ADA38174
27	20.4	81.6	25	10	AAD60570
28	20.4	81.6	25	10	ACC44662
29	20.4	81.6	25	12	ADL93428
30	20.4	81.6	48	3	AAC55543
31	20.4	81.6	48	3	AAC55568
32	20.4	81.6	48	3	AAS06244
33	20.4	81.6	48	4	AAS06244
34	20.4	81.6	48	4	AAS06215
35	20	80.0	25	2	AAH78942
36	20	80.0	25	3	AAC55381
37	20	80.0	25	4	AAS06182
38	20	80.0	25	4	AAC87900
39	20	80.0	25	4	AAF55769
40	20	80.0	25	4	AH22543
41	20	80.0	25	4	AAD14460
42	20	80.0	25	9	ACD28430
43	20	80.0	25	9	ACD28609
44	20	80.0	25	9	ADA38196
45	20	80.0	25	10	ADF42420

ALIGNMENTS

RESULT 1

AAT48213
ID AAT48213 standard; DNA; 25 BP.

AC AAT48213;

DT 20-OCT-1997 (first entry)

DE M-attL core region.

KW att recombination site; core region; mutation; enhance; recombination;
KW vector; subcloning; regulation; exchange; ss.

OS Synthetic.

XX WO9640724-A1.

PD 19-DEC-1996.

PF 07-JUN-1996; 96WO-US010082.

PR 07-JUN-1995; 95US-00486139.

XX (LIFE-) LIFE TECHNOLOGIES INC.

PI Hartley JL, Brasch MA;

XX WPI; 1997-065168/06.

PT Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
PT using recombinant proteins and engineered recombination sites in vitro or
PT in vivo.

XX Claim 14; Page 55; 106pp; English.

XX AAT48210-25 are att recombination site core region DNA sequences. The
XX core region has at least one engineered mutation that enhances
XX recombination in vitro in the formation of a co-integrate or Product DNA.
XX These core regions can be incorporated into novel vector donor DNA
XX molecules. The nucleic acids, vectors and methods of the invention are
XX used to obtain chimeric nucleic acid using recombination proteins and
XX engineered recombination sites in vitro or in vivo. The improved
XX specificity, speed and yields of the invention facilitates DNA or RNA
XX subcloning, regulation or exchange useful for any related purpose, e.g.

CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
CC or modification of transcribed, replicated, isolated or genomic DNA or
CC RNA

XX Sequence 25 BP; 4 A; 5 C; 4 G; 6 T; 0 U; 6 Other;

Query Match 86.4%; Score 21.6; DB 2; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.68;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCGCTTCTCTACNAAGTSG 25

Db 1 AGCCGCTTCTCTACNAAGTSG 25

RESULT 2

AAX78938

ID AAX78938 standard; DNA; 25 BP.

XX

AC AAX78938;

XX

DT 17-AUG-1999 (first entry)

XX

DE Oligonucleotide #4 for recombination and cloning method.

XX

KW Cloning; donor; recombination site; vector; chimeric; ss.

XX

OS Synthetic.

XX

PN WO9921977-A1.

XX

PD 06-MAY-1999.

XX

PF 26-OCT-1998; 98WO-US022589.

XX

PR 24-OCT-1997; 97US-0065930P.

XX

PR 23-OCT-1998; 98US-00177387.

XX

PA (LIFE-) LIFE TECHNOLOGIES INC.

XX

PI Hartley JL, Brasch MA, Temple GF, Fox DK;

XX

DR WPI; 1999-303011/25.

XX

PT New nucleic acid cloning methods.

XX

PS Disclosure; Page 159; 185pp; English.

XX

CC The invention relates to novel methods for cloning or subcloning one or
CC more nucleic acid molecules (NMs) comprising: (a) combining in vitro or
CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
CC more desired nucleic acid segments flanked by at least 2 recombination
CC sites which do not recombine with each other; (2) one or more vector
CC donor molecules (VDMs) comprising at least 2 recombination sites which do
CC not recombine with each other; and (3) one or more site-specific
CC recombination proteins; (b) incubating the combination to transfer one or
CC more of the desired segments into one or more of the VDMs, thereby
CC producing one or more desired product molecules (PMs). The methods can be
CC used for the efficient and specific recombination of NAM segments. They
CC can be used to generate chimeric DNA or RNA molecules that have the
CC desired characteristics and/or nucleic acid segments. The methods can
CC also be used for changing vectors. The oligonucleotides AAX78935-X78994
CC are used in the method of the invention

XX Sequence 25 BP; 4 A; 5 C; 4 G; 6 T; 0 U; 6 Other;

Query Match 86.4%; Score 21.6; DB 2; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.68;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCGCTTCTCTACNAAGTSG 25

Db 1 AGCCGCTTCTCTACNAAGTSG 25

RESULT 3

AAC87869

ID AAC87869 standard; DNA; 25 BP.

XX

AC AAC87869;

XX

DT 02-MAR-2001 (first entry)

XX

DE Escherichia coli core region recombinant site m-attL SEQ ID NO:4.

XX

KW Core region; recombination site; cloning; chimeric DNA; characteristic;
mutation; att site; lox site; ss.

XX

OS Escherichia coli.

XX

PN US6143557-A.

XX

PD 07-NOV-2000.

XX

PF 20-JAN-1999; 99US-00233493.

XX

PR 07-JUN-1995; 95US-00486139.

XX

PR 07-JUN-1996; 96US-00663002.

XX

PR 12-JAN-1998; 98US-00005476.

XX

PA (LIFE-) LIFE TECHNOLOGIES INC.

XX

PI Brasch MA, Hartley JL;

XX

DR WPI; 2001-049004/06.

XX

PT Isolated nucleic acid molecules comprising a DNA segment having two
engineered recombination sites, derived from att or lox, which flank a
selectable marker and comprise a core region having an engineered
mutation.

XX

PS Claim 1; Col 18; 73pp; English.

XX

CC The present invention describes an isolated nucleic acid molecule (I)
comprising a first nucleic acid sequence having a defined sequence
(AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,
or an RNA sequence corresponding to AAC87866 to AAC87881. Also described
are: (1) an isolated nucleic acid molecule (II) comprising a first
mutated recombination site that removes one or more stop codons from the
recombination site or avoids hairpin formation, the recombination site
being an att or lox site; (2) an isolated nucleic acid molecule (III)
comprising a first att recombination site comprising a mutation that
enhances recombination specificity; (3) vectors (IV) comprising the above
mentioned nucleic acids; and (4) cells comprising the above mentioned
nucleic acids or (IV). The nucleic acids are used in engineering a core
region of a given recombination site to provide mutative sites suitable
for subcloning reactions. The use of nucleic acids for obtaining
engineered recombination in vitro or in vivo makes the methods for DNA or
RNA subcloning, highly specific, rapid, and less labour intensive

XX Sequence 25 BP; 4 A; 5 C; 4 G; 6 T; 0 U; 6 Other;

Query Match 86.4%; Score 21.6; DB 4; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.68;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCGCTTCTCTACNAAGTSG 25

Db 1 AGCCGCTTCTCTACNAAGTSG 25

RESULT 4

AAF55738

ID AAF55738 standard; DNA; 25 BP.

XX

AC AAF55738;


```

XX 12-APR-2001 (first entry)
XX DT
XX Recombination site m-attL.
XX DE
XX Recombination site; cloning; m-att; ss.
XX KW
XX Unidentified.
XX OS
XX US6171861-B1.
XX PN
XX 09-JAN-2001.
XX PD
XX 12-JAN-1998; 98US-00005476.
XX PF
XX 07-JUN-1995; 95US-00486139.
XX PR
XX 07-JUN-1996; 96US-00663002.
XX PA
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX PI
XX Hartley JL, Brasch MA;
XX WPI; 2001-136877/14.
XX DR
XX In vitro cloning of nucleic acid involves mixing vectors comprising
XX PT recombination sites and/or nucleic acid, incubating mixture to produce
XX PT chimeric molecule, contacting hosts with mixture and selecting host.
XX PT
XX Claim 24; Col 46; 73pp; English.
XX PS
XX The present invention relates to a method for in vitro cloning of a
XX CC nucleic acid of interest. The method involves mixing in vitro two vectors
XX CC each comprising at least one recombination site and the nucleic acid of
XX CC interest; incubating the mixture in the presence of at least one
XX CC recombination protein to result in recombination of the recombination
XX CC sites, leading to production of a chimeric nucleic acid molecule
XX CC comprising the nucleic acid of interest; contacting hosts with the
XX CC mixture; and selecting for a host comprising the chimeric nucleic acid
XX CC molecule, and selecting against a host comprising the vectors comprising
XX CC the second vector, to clone the nucleic acid. The present sequence is a
XX CC recombination site, which may be used in the method of the present
XX CC invention
XX SQ
XX Sequence 25 BP; 4 A; 5 C; 4 G; 6 T; 0 U; 6 Other;

Query Match      86.4%; Score 21.6; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTCTKTRTACNAAGTSG 25
   |||||
Db 1 AGCCWGCCTTCTKTRTACNAAGTSG 25

RESULT 5
AADI4432
ID AADI4432 standard; DNA; 25 BP.
XX
XX AADI4432;
XX AC
XX 01-NOV-2001 (first entry)
XX DT
XX Recombination site m-attL DNA.
XX DE
XX Recombination site; copy number; replicon; recombinatorial cloning;
XX KW m-attL; ds.
XX KW
XX Unidentified.
XX OS
XX US6270969-B1.
XX PN
XX 07-AUG-2001.
XX PD
XX

XX 20-JAN-1999; 99US-00233492.
XX PF
XX 07-JUN-1995; 95US-00486139.
XX PR
XX 07-JUN-1996; 96US-00663002.
XX XX
XX (INVI-) INVITROGEN CORP.
XX PA
XX Hartley JL, Brasch MA;
XX PI
XX WPI; 2001-488248/53.
XX DR
XX Methods for apposing nucleic acids comprising an expression signal and a
XX PF gene/partial gene, using recombinatorial cloning by incubating the
XX PT nucleic acids in the presence of a recombination protein under conditions
XX PT for recombination.
XX PT
XX Claim 14; Col 18; 76pp; English.
XX PS
XX The invention relates to a method for apposing an expression signal and a
XX CC gene or partial gene, using recombinatorial cloning. The method incubates
XX CC nucleic acids comprising the expression signal and the gene/partial gene
XX CC in the presence of a recombination protein under conditions sufficient to
XX CC cause recombination and therefore appose the expression signal and the
XX CC gene or partial gene. The methods are useful for apposing an expression
XX CC signal and a gene or partial gene using recombinatorial cloning. The
XX CC methods are also useful for changing vectors, constructing genes for
XX CC fusion proteins, changing copy number, changing replicons, cloning into
XX CC phages, and cloning e.g., PCR products (with an attB site at one end and
XX CC a loxP site at the other end), genomic DNAs, and cDNAs. The methods are
XX CC highly specific, rapid, and less labour intensive than prior art methods.
XX CC The present sequence is a recombination site useful for recombination
XX CC cloning
XX SQ
XX Sequence 25 BP; 4 A; 5 C; 4 G; 6 T; 0 U; 6 Other;

Query Match      86.4%; Score 21.6; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTCTKTRTACNAAGTSG 25
   |||||
Db 1 AGCCWGCCTTCTKTRTACNAAGTSG 25

RESULT 6
AASI4783
ID AASI4783 standard; DNA; 25 BP.
XX
XX AASI4783;
XX AC
XX 27-FEB-2002 (first entry)
XX DT
XX Lambda phage Int recombinase site core region DNA sequence m-attL.
XX DE
XX Recombinant nucleic acid vector; carcinoembryonic antigen; CEA; cytokine;
XX KW syncytium-inducing polypeptide; fusogenic membrane glycoprotein; tumour;
XX KW recombinase; tumour-specific promoter; hypoxic response element; HRE; ss;
XX KW tyrosinase promoter; Cre; FLP; retroviral vector; malignant cell; cancer;
XX KW cytosstatic; gene therapy; Int recombinase site core region; m-attL;
XX KW excisive recombination.
XX KW
XX Bacteriophage lambda.
XX OS
XX WO200174861-A2.
XX PN
XX 11-OCT-2001.
XX PD
XX 30-MAR-2001; 2001WO-US010250.
XX PF
XX 31-MAR-2000; 2000US-0193977P.
XX PR
XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
XX PA
XX

```

PI Vile RG, Harrington K, Murphy S, Bateman A;
 XX WPI; 2001-656985/75.
 XX
 PT Recombinant nucleic acid vector for reducing tumor size, has expression
 PT cassette comprises a promoter linked to nucleic acid sequence encoding a
 PT syncytium-inducing polypeptide and flanked on either side by recombinase.
 XX
 PS Disclosure; Page 42; 84pp; English.
 XX
 CC The invention relates to a recombinant nucleic acid vector comprising a
 CC first expression cassette, comprising a first promoter operably linked to
 CC a nucleic acid sequence encoding a syncytium-inducing polypeptide (such
 CC as a fusogenic membrane glycoprotein) and flanked on either side by a
 CC sequence recognised by a recombinase, and/or a second expression cassette
 CC comprising a tumour-specific promoter operably linked to a nucleic acid
 CC sequence encoding a recombinase. The nucleic acid of the first expression
 CC cassette may be linked to a hypoxic response element (HRE), the second
 CC expression cassette may contain a promoter linked to a nucleic acid
 CC encoding a cytokine, and a third cassette may contain a tumour specific
 CC promoter linked to the nucleic acid encoding the recombinase. The tumour
 CC specific promoter is, for example, a carcinoembryonic antigen (CEA)
 CC promoter or a tyrosinase promoter and the recombinase is, for example,
 CC Cre recombinase or Flp recombinase. The invention is useful for reducing
 CC tumour size by administering the compositions as retroviral vectors, or
 CC in a cell containing the vector, to an individual in need of treatment
 CC for a disease caused by malignant cells. This sequence represents an Int
 CC recombinase site core region m-attL, required for exciseive recombination
 XX
 SQ Sequence 25 BP; 4 A; 5 C; 4 G; 6 T; 0 U; 6 Other;
 Query Match 86.4%; Score 21.6; DB 5; Length 25;
 Best Local Similarity 100.0%; Pred. NO. 0.68;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGCCGCTTCTCKTRTACNAAGTSGB 25
 Db 1 AGCCGCTTCTCKTRTACNAAGTSGB 25
 RESULT 7
 ABT16624
 ID ABT16624 standard; DNA; 25 BP.
 XX
 AC ABT16624;
 XX
 DT 03-APR-2003 (first entry)
 XX
 DE Artificial plant chromosome related oligo SEQ ID No 36.
 XX
 KW Plant artificial chromosome; PAC; transgenic plant; vaccine;
 KW blood factor; herbicide; stress; agronomical; nutrient quality;
 KW bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
 KW ds.
 XX
 OS Unidentified.
 XX
 PN WO200296923-A1.
 XX
 PD 05-DEC-2002.
 XX
 PF 30-MAY-2002; 2002WO-US017451.
 XX
 PR 30-MAY-2001; 2001US-0294687P.
 PR 04-JUN-2001; 2001US-0296329P.
 XX
 PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
 PA (AGRI-) AGRISOMA INC.
 XX
 PI Perez C, Fabijanski SF, Perkins E;
 XX
 DR WPI; 2003-140436/13.
 XX

PT Producing artificial chromosome by introducing a nucleic acid into plant
 PT cell, selecting artificial chromosome that has one or more repeat regions
 PT with equivalent amounts of euchromatic and heterochromatic nucleic acids.
 XX
 PS Disclosure; Page 261; 269pp; English.
 XX
 CC The invention relates to a novel method for producing plant artificial
 CC chromosomes. The invention also relates to methods for targeting
 CC insertion of heterologous DNA into plant artificial chromosomes, methods
 CC for delivery of plant chromosomes to selected cells and tissues. The
 CC isolated plant artificial chromosome (PAC) is useful for producing a
 CC transgenic plant, which involves introducing the PAC into a plant cell.
 CC The PAC comprises a heterologous nucleic acid encoding a gene product
 CC such as enzymes, antisense RNA, rRNA, tRNA, structural proteins, marker
 CC proteins, ligands, receptors, ribozymes, therapeutic proteins, and
 CC biopharmaceutical proteins, vaccines, blood factors, antigens, hormones,
 CC cytokines, growth factors, antibodies, or a product that provides for
 CC resistance to diseases, insects, herbicides, or stress in a plant. The
 CC heterologous nucleic acid optionally encodes a product that provides an
 CC agronomically important trait in the plant, e.g. a product that alters
 CC nutrient use and/or improves the nutrient quality of the plant. The
 CC heterologous nucleic acid is contained within a bacterial artificial
 CC chromosome (BAC) or a yeast artificial chromosome (YAC). This
 CC polynucleotide sequence represents an oligo relating to the method for
 CC producing plant artificial chromosomes of the invention
 XX
 SQ Sequence 25 BP; 4 A; 5 C; 4 G; 6 T; 0 U; 6 Other;
 Query Match 86.4%; Score 21.6; DB 8; Length 25;
 Best Local Similarity 100.0%; Pred. NO. 0.68;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGCCGCTTCTCKTRTACNAAGTSGB 25
 Db 1 AGCCGCTTCTCKTRTACNAAGTSGB 25
 RESULT 8
 ACD28279
 ID ACD28279 standard; DNA; 25 BP.
 XX
 AC ACD28279;
 XX
 DT 02-OCT-2003 (first entry)
 XX
 DE Nucleic acid core region m-attL.
 XX
 KW Core region; ds; vector donor DNA; flanking recombination site; m-attL.
 XX
 OS Synthetic.
 XX
 PN US2003064515-A1.
 XX
 PD 03-APR-2003.
 XX
 PF 30-JAN-2002; 2002US-00058291.
 XX
 PR 07-JUN-1995; 95US-00486139.
 PR 07-JUN-1996; 96US-00663002.
 PR 20-JAN-1999; 99US-00233493.
 PR 02-NOV-1999; 99US-00432085.
 XX
 PA (HART/) HARTLEY J L.
 PA (BRAS/) BRASCH M A.
 XX
 PI Hartley JL, Brasch MA;
 XX
 DR WPI; 2003-540791/51.
 XX
 PT New Vector Donor DNA molecule for recombinational cloning using
 PT engineered recombination sites, comprises first and second DNA segments
 PT that do not recombine with each other and that contain a Selectable
 PT marker.

XX Claim 14; Page 25; 71pp; English.

PS The invention relates to a vector donor DNA molecule comprising a first

CC DNA segment and a second DNA segment containing at least one selectable

CC marker. The first and second segments are separated either by, in a

CC circular vector donor, a first and a second recombination site, or in a

CC linear vector donor, at least a first recombination site, where each pair

CC of flanking recombination sites are engineered and do not recombine with

CC each other. The nucleic acid molecule, vectors and methods are useful for

CC moving or exchanging segments of DNA molecules using engineered

CC recombination sites and recombination proteins to provide chimeric DNA

CC molecules that have the desired characteristic(s) and/or DNA segment(s).

CC The present sequence represents the nucleic acid core region m-attL

XX Sequence 25 BP; 4 A; 5 C; 4 G; 6 T; 0 U; 6 Other;

SQ

Query Match 86.4%; Score 21.6; DB 9; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.68;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCGCGCTTCTCKTRTACNAAGTSG 25

Db 1 AGCCGCGCTTCTCKTRTACNAAGTSG 25

RESULT 9

ID ACD28479 standard; DNA; 25 BP.

XX ACD28479;

AC

XX 09-OCT-2003 (first entry)

DT

XX Nucleic acid core sequence m-attL.

DE

XX Nucleic acid core; m-attL; cointegrate DNA; flanking recombination site;

KW ds.

XX Synthetic.

OS

XX US2003068799-A1.

PN

XX 10-APR-2003.

PD

XX 06-JUN-2002; 2002US-00162879.

PF

XX 07-JUN-1995; 95US-00486139.

PR

XX 07-JUN-1996; 96US-00663002.

PR

XX 20-JAN-1999; 99US-00233493.

PR

XX 02-NOV-1999; 99US-00432085.

XX (INVI-) INVITROGEN CORP.

PA

XX Hartley JL, Brasch MA;

PI

XX WPI; 2003-540884/51.

DR

XX Making Cointegrate DNA molecule, by combining recombination sites

PT flanking the desired DNA segment in insert donor DNA, with the

PT recombination sites of vector donor DNA, using site specific

PT recombination protein.

PS Claim 14; Page 25; 71pp; English.

XX The invention relates to a method of making a cointegrate DNA molecule.

CC The method is useful for making a cointegrate DNA molecule. The method is

CC useful for a variety of DNA exchanges, such as subcloning of DNA, in

CC vitro or in vivo. The method enables efficient and specific recombination

CC of DNA segments using recombination proteins. The method is highly

CC specific, rapid and less labour intensive. The improved specificity,

CC yield and speed of the method facilitates DNA or RNA subcloning,

CC regulation and exchange useful for other related purposes. Since single

CC

CC molecules of the recombinations product can be introduced into a

CC biological host, propagation of the desired product DNA in the absence of

CC other DNA molecules is more readily realised. Reaction conditions can be

CC freely adjusted in vitro to optimise enzyme activities. The present

CC sequence represents the nucleic acid core sequence m-attL

XX Sequence 25 BP; 4 A; 5 C; 4 G; 6 T; 0 U; 6 Other;

SQ

Query Match 86.4%; Score 21.6; DB 9; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.68;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCGCGCTTCTCKTRTACNAAGTSG 25

Db 1 AGCCGCGCTTCTCKTRTACNAAGTSG 25

RESULT 10

ID ADA38165 standard; DNA; 25 BP.

XX ADA38165;

AC

XX 20-NOV-2003 (first entry)

DT

XX m-attL DNA sequence indicating generic core region of an attL site.

DE

XX engineered recombination site; cloning; recombinase; subcloning; attB;

KW attP; attL; attR; selectable marker; cointegrate; m-attL; ds.

XX Synthetic.

OS

XX US2003054552-A1.

PN

XX 20-MAR-2003.

PD

XX 30-JAN-2002; 2002US-00058292.

PF

XX 07-JUN-1995; 95US-00486139.

PR

XX 07-JUN-1996; 96US-00663002.

PR

XX 20-JAN-1999; 99US-00233493.

PR

XX 02-NOV-1999; 99US-00432085.

XX (HARTLEY) HARTLEY J L.

PA

XX (BRASCH) BRASCH M A.

PI

XX Hartley JL, Brasch MA;

XX WPI; 2003-585168/55.

DR

XX New Vector Donor DNA molecule, useful for recombinational cloning

PT purposes, comprises a first and a second DNA segment that contains a

PT selectable marker and is separated by a pair of flanking, engineered

PT recombination sites.

PS Claim 14; Page 26; 72pp; English.

XX This invention relates to novel DNA and vectors having engineered

CC recombination sites for use in a cloning method that enables efficient

CC and specific recombination of DNA segments using recombination proteins

CC including recombinases. As such, it provides a method for obtaining

CC chimeric nucleic acids with the desired characteristics, facilitating DNA

CC or RNA subcloning, regulation and/or exchange. The recombination site is

CC derived from attB attP, attL or attR, where the att site is attI, att2 or

CC att3. Engineered mutations of the att sites (either one or multiple

CC mutations) can enhance specificity or efficiency of the recombination

CC reaction and the properties of the product DNA molecules. Accordingly,

CC the present invention describes a nucleic acid molecule comprising at

CC least one DNA segment having at least two engineered recombination sites

CC flanking a selectable marker and/or a desired DNA segment. Furthermore,

CC at least one of the engineered sites must enhance recombination in vitro

CC to form a cointegrate or product DNA molecule. This oligonucleotide

CC sequence is m-attL, a generic DNA sequence indicating the core region of

```

CC an attL recombination site of the invention.
SQ Sequence 25 BP; 4 A; 5 C; 4 G; 6 T; 0 U; 6 Other;

  Query Match      86.4%; Score 21.6; DB 9; Length 25;
  Best Local Similarity 100.0%; Pred. No. 0.68;
  Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTCKTRTACNAAGTSG 25
   |||||
Db 1 AGCCWGCCTTCKTRTACNAAGTSG 25

RESULT 11
AAD60561
ID AAD60561 standard; DNA; 25 BP.
XX
AC AAD60561;
XX
XX 18-DEC-2003 (first entry)
XX
XX Core region DNA, m-attL.
XX
XX Recombinational cloning; DNA exchange; core region; ds.
XX
XX Unidentified.
XX
XX US2003100110-A1.
XX
XX 29-MAY-2003.
XX
XX 02-NOV-1999; 99US-00432085.
XX
XX 07-JUN-1995; 95US-00486139.
XX
XX 07-JUN-1996; 96US-00663002.
XX
XX 20-JAN-1999; 99US-00233493.
XX
XX (HARTLEY J L.
XX (BRASCH M A.
XX
XX Hartley JL, Brasch MA;
XX
XX WPI; 2003-730143/69.
XX
XX New Vector Donor DNA molecule for recombinational cloning using
XX engineered recombination sites, comprises first and second DNA segments
XX that do not recombine with each other and that contain a Selectable
XX marker.
XX
XX Claim 14; Page 25; 71pp; English.
XX
XX The invention relates to a vector donor DNA molecule which comprises
XX first and second DNA segments that do not recombine with each other and
XX that contain a selectable marker. The invention also relates to a method
XX for recombinational cloning using engineered recombination sites. The
XX invention is useful for moving or exchanging segments of DNA molecules
XX using engineered recombination sites and recombination proteins to
XX provide chimeric DNA molecules that have the desired characteristic(s)
XX and/or DNA segment(s). The present sequence is a core region DNA. This
XX sequence is used to illustrate the method of the invention
XX
XX Sequence 25 BP; 4 A; 5 C; 4 G; 6 T; 0 U; 6 Other;

  Query Match      86.4%; Score 21.6; DB 10; Length 25;
  Best Local Similarity 100.0%; Pred. No. 0.68;
  Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTCKTRTACNAAGTSG 25
   |||||
Db 1 AGCCWGCCTTCKTRTACNAAGTSG 25

RESULT 12
AAD60561
ID AAD60561 standard; DNA; 25 BP.
XX
AC AAD60561;
XX
XX 29-MAY-2003 (first entry)
XX
XX Recombination site related oligonucleotide SEQ ID NO:44.
XX
XX Chromosome-based platform; artificial chromosome; eukaryotic chromosome;
XX att site; integrase; recombinase; ACes; gene therapy; transgenic animal;
XX platform artificial chromosome expression system; PCR primer; ss.
XX
XX Synthetic.
XX
XX WO200297059-A2.
XX
XX 05-DEC-2002.
XX
XX 30-MAY-2002; 2002WO-US017452.
XX
XX 30-MAY-2001; 2001US-0294758P.
XX
XX 21-MAR-2002; 2002US-0366891P.
XX
XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
XX
XX Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;
XX Stewart S, Shellard J;
XX
XX WPI; 2003-140461/13.
XX
XX Novel eukaryotic chromosome comprising one or many att sites which
XX permits site-directed integration in the presence of lambda-integrase,
XX useful for site-specific recombination-directed integration of DNA of
XX interest.
XX
XX Claim 43; Page 143; 272pp; English.
XX
XX The present invention describes a eukaryotic chromosome (I) comprising
XX one or several att sites, where an att site is heterologous to the
XX chromosome, and permits site-directed integration in the presence of
XX lambda-integrase. Also described: (I) a platform artificial chromosome
XX expression system (ACes) (II) comprising several sites that participate
XX in recombinase catalysed recombination; and (2) a method (M1) for
XX introducing a heterologous nucleic acid into a platform artificial
XX chromosome. (I) can be used in gene therapy. (M1) is useful for
XX introducing a heterologous nucleic acid molecule into a platform
XX artificial chromosome, preferably an ACes. (II) is useful for producing a
XX transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or
XX mammal) by introducing (II) by cell fusion, lipid-mediated transfection
XX by a carrier system, microinjection, microcell fusion, electroporation,
XX microprojectile bombardment or direct DNA transfer into an embryonic
XX cell, preferably a stem cell or an embryo. (II) comprises a heterologous
XX nucleic acid that encodes a therapeutic product which is useful for
XX making a library of ACes comprising random portions of a genome. ACC44612
XX to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
XX exemplification of the present invention
XX
XX Sequence 25 BP; 4 A; 5 C; 4 G; 6 T; 0 U; 6 Other;

  Query Match      86.4%; Score 21.6; DB 10; Length 25;
  Best Local Similarity 100.0%; Pred. No. 0.68;
  Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTCKTRTACNAAGTSG 25
   |||||
Db 1 AGCCWGCCTTCKTRTACNAAGTSG 25

RESULT 13
ADL93419
ID ADL93419 standard; DNA; 25 BP.
XX

```


DE	attL2 core region.	
XX		
KW	att recombination site; core region; mutation; enhance; recombination;	
KW	vector; subcloning; regulation; exchange; ss.	
XX		
OS	Synthetic.	
XX		
FN	WO9640724-A1.	
XX		
PD	19-DEC-1996.	
XX		
XX	07-JUN-1996; 96WO-US010082.	
XX		
PR	07-JUN-1995; 95US-00486139.	
XX		
PA	(LIFE-) LIFE TECHNOLOGIES INC.	
XX		
PI	Hartley JL, Brasch MA;	
XX		
XX	WPI; 1997-065168/06.	
DR		
XX		
XX	Nucleic acids, vectors and methods to obtain chimeric nucleic acid -	
PT	using recombinant proteins and engineered recombination sites in vitro or	
PT	in vivo.	
XX		
XX	Claim 14; Page 56; 106pp; English.	
PS		
XX		
CC	AT48210-25 are att recombination site core region DNA sequences. The	
CC	core region has at least one engineered mutation that enhances	
CC	recombination in vitro in the formation of a Cointegrate or Product DNA.	
CC	These core regions can be incorporated into novel vector donor DNA	
CC	molecules. The nucleic acids, vectors and methods of the invention are	
CC	used to obtain chimeric nucleic acid using recombination proteins and	
CC	engineered recombination sites in vitro or in vivo. The improved	
CC	specificity, speed and yields of the invention facilitates DNA or RNA	
CC	subcloning, regulation or exchange useful for any related purpose, e.g.	
CC	in vitro recombination of DNA segments, and in vitro or in vivo insertion	
CC	or modification of transcribed, replicated, isolated or genomic DNA or	
CC	RNA	
XX		
SQ	Sequence 25 BP; 5 A; 5 C; 6 G; 9 T; 0 U; 0 Other;	
	Query Match 81.6%; Score 20.4; DB 2; Length 25;	
	Best Local Similarity 76.0%; Pred. No. 2.7;	
	Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;	
Qy	1 AGCCWGCCTTCTKTRTACNAAGTSGB 25	
	: : :	
Db	1 AGCGTCTTCTTGTAACAAATTGG 25	

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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:19 ; Search time 35.9 Seconds
(without alignments)
494.978 Million cell updates/sec

Title: US-10-820-133-4

Perfect score: 25

Sequence: 1 agcwggttcttactnaagtsbp 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

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4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21.6	86.4	25	3	US-09-233-493-4
2	21.6	86.4	25	3	US-09-005-476-4
3	21.6	86.4	25	3	US-09-233-492-4
4	21.6	86.4	25	3	US-09-296-280-4
5	21.6	86.4	25	4	US-09-498-074-4
6	21.6	86.4	25	4	US-09-498-074-4
7	21.6	86.4	25	5	PCT-US96-10082A-4
8	20.4	81.6	25	3	US-09-233-493-13
9	20.4	81.6	25	3	US-09-005-476-13
10	20.4	81.6	25	3	US-09-233-492-13
11	20.4	81.6	25	3	US-09-296-280-13
12	20.4	81.6	25	3	US-09-296-280-40
13	20.4	81.6	25	4	US-09-498-074-13
14	20.4	81.6	25	4	US-09-498-074-13
15	20.4	81.6	25	5	PCT-US96-10082A-13
16	20.0	80.0	25	3	US-09-233-493-35
17	20.0	80.0	25	3	US-09-005-476-35
18	20.0	80.0	25	3	US-09-233-492-35
19	20.0	80.0	25	3	US-09-296-280-8
20	20.0	80.0	25	4	US-09-498-074-35
21	20.0	80.0	25	4	US-09-498-074-35
22	20.0	80.0	46	3	US-09-296-280-51
23	20.0	80.0	47	3	US-09-296-280-57
24	20.0	80.0	49	4	US-09-935-916B-64
25	20.0	80.0	49	4	US-09-935-916B-65
26	20.0	80.0	49	4	US-09-935-916B-66
27	20.0	80.0	50	3	US-09-296-280-53

Sequence 59, Appl
Sequence 13, Appl
Sequence 16, Appl
Sequence 1013, Ap
Sequence 968, App
Sequence 964, App
Sequence 99, Appl
Sequence 12, Appl
Sequence 109, App
Sequence 109, App
Sequence 970, App
Sequence 419, App
Sequence 373, App
Sequence 276, App
Sequence 742, App
Sequence 100, App
Sequence 101, App
Sequence 101, App

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US-09-620-312D-1013
US-09-620-312D-968
US-09-620-312D-964
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US-09-620-312D-970
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US-09-620-312D-742
US-09-620-312D-100
US-09-620-312D-101
US-09-620-312D-101

ALIGNMENTS

RESULT 1
US-09-233-493-4
; Sequence 4, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-493-4

Query Match 86.4%; Score 21.6; DB 3; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.055;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCGCGCTTCTKTRTACNAAGTSG 25
 |||||
 Db 1 AGCCGCGCTTCTKTRTACNAAGTSG 25

RESULT 5

US-09-498-074-4
 ; Sequence 4, Application US/09498074
 ; Patent No. 6534264
 ; GENERAL INFORMATION:
 ; APPLICANT: Hartley, James L.
 ; APPLICANT: Brach, Michael A.
 ; TITLE OF INVENTION: Recombinational Cloning Using Engineered
 ; RECOMBINATION SITES
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
 ; STREET: 1100 New York Ave., N. W. Suite 600
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/498,074
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/005,476
 ; FILING DATE: 12-JAN-1998
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/663,002
 ; FILING DATE: 07-JUN-1996
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/486,139
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2540
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 25 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: both
 ; MOLECULE TYPE: CDNA
 ; US-09-498-074-4

Query Match 86.4%; Score 21.6; DB 4; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.055;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCGCGCTTCTKTRTACNAAGTSG 25
 |||||
 Db 1 AGCCGCGCTTCTKTRTACNAAGTSG 25

RESULT 6

US-09-498-074-4
 ; Sequence 4, Application US/09498074
 ; Patent No. 6720140
 ; GENERAL INFORMATION:

APPLICANT: Hartley, James L.
 APPLICANT: Brach, Michael A.
 TITLE OF INVENTION: Recombinational Cloning Using Engineered
 RECOMBINATION SITES

NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
 STREET: 1100 New York Ave., N. W. Suite 600
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-3934

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
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 SOFTWARE: Patentin Release #1.0, Version #1.30
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 APPLICATION NUMBER: US/09/498,074
 FILING DATE: 04-Feb-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/005,476
 FILING DATE: 12-JAN-1998
 APPLICATION NUMBER: 08/663,002
 FILING DATE: 07-JUN-1996
 APPLICATION NUMBER: 08/486,139
 FILING DATE: 07-JUN-1995
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both
 MOLECULE TYPE: CDNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-09-498-074-4

Query Match 86.4%; Score 21.6; DB 4; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.055;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCGCGCTTCTKTRTACNAAGTSG 25
 |||||
 Db 1 AGCCGCGCTTCTKTRTACNAAGTSG 25

RESULT 7

PCT-US96-10082A-4
 ; Sequence 4, Application PC/TUS9610082A
 ; GENERAL INFORMATION:
 ; APPLICANT: Life Technologies, Inc.
 ; APPLICANT: 8717 Grovemont Circle
 ; APPLICANT: Gaithersburg, MD 20884-9980
 ; APPLICANT: United States of America
 ; APPLICANT: Brach, Michael A.
 ; TITLE OF INVENTION: Recombinational Cloning Using Engineered
 ; RECOMBINATION SITES
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
 ; STREET: 1100 New York Ave., N. W. Suite 600
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US96/10082A
;; FILING DATE: 07-JUN-1996
;; CLASSIFICATION:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 25 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; MOLECULE TYPE: cdna
PCT-US96-10082A-4

Query Match 86.4%; Score 21.6; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCWGCCTTCTKTRTACNAAGTSGB 25
|||||
DB 1 AGCCWGCCTTCTKTRTACNAAGTSGB 25

RESULT 8
US-09-233-493-13
; Sequence 13, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both

;; MOLECULE TYPE: cdna
US-09-233-493-13

Query Match 81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.23;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGCCWGCCTTCTKTRTACNAAGTSGB 25
|||||
DB 1 AGCCGCTTCTTGTACAAAGTTGG 25

RESULT 9
US-09-005-476-13
; Sequence 13, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-13

Query Match 81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.23;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGCCWGCCTTCTKTRTACNAAGTSGB 25
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DB 1 AGCCGCTTCTTGTACAAAGTTGG 25

RESULT 10
US-09-233-492-13
; Sequence 13, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
;; STREET: 1100 New York Ave., N. W. Suite 600
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005-3934
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/233,492
;; FILING DATE: 20-JAN-1999
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/663,002
;; FILING DATE: 07-JUN-1996
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/486,139
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 25 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; MOLECULE TYPE: cdna
;; US-09-233-492-13

Query Match 81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.23; Indels 0; Gaps 0;
Matches 19; Conservative 4; Mismatches 2;

Qy 1 AGCCGCTTTCTKTRTACNAAGTSG 25
Db 1 AGCCTGCTTTCTGTACAAAGTTGG 25

RESULT 11
US-09-296-280-13
; Sequence 13, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
US-09-296-280-13

Query Match 81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.23; Indels 0; Gaps 0;
Matches 19; Conservative 4; Mismatches 2;

Qy 1 AGCCGCTTTCTKTRTACNAAGTSG 25
Db 1 AGCCTGCTTTCTGTACAAAGTTGG 25

RESULT 12
US-09-296-280-40
; Sequence 40, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
US-09-296-280-40

Query Match 81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 72.0%; Pred. No. 0.23; Indels 0; Gaps 0;
Matches 18; Conservative 6; Mismatches 1;

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Db 1 ASCCGCTTTTTRTACWAAATGKM 25

RESULT 13
US-09-498-074-13
; Sequence 13, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:

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/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/005,476
/ FILING DATE: 12-JAN-1998
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/663,002
/ FILING DATE: 07-JUN-1996
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/486,139
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION:
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: both
/ MOLECULE TYPE: cdna
US-09-498-074-13

Query Match      81.6%; Score 20.4; DB 4; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.23;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGCCGCTTTCTKTRTACNAAGTSGB 25
Db 1 AGCCGCTTTCTTGACAAAGTTGG 25

RESULT 14
US-09-498-074-13
/ Sequence 13, Application US/09498074
/ Patent No. 6720140
/ GENERAL INFORMATION:
/ APPLICANT: Hartley, James L.
/ BRASCH, Michael A.
/ TITLE OF INVENTION: Recombinational Cloning Using Engineered
/ RECOMBINATION SITES
/ NUMBER OF SEQUENCES: 35
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
/ STREET: 1100 New York Ave., N. W. Suite 600
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3934
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/498,074
/ FILING DATE: 04-Feb-2000
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/005,476
/ FILING DATE: 12-JAN-1998
/ APPLICATION NUMBER: 08/663,002
/ FILING DATE: 07-JUN-1996
/ APPLICATION NUMBER: 08/486,139
/ FILING DATE: 07-JUN-1995
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 base pairs
/ TYPE: nucleic acid
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/ STRANDEDNESS: both
/ TOPOLOGY: both
/ MOLECULE TYPE: cdna
/ SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-498-074-13

Query Match      81.6%; Score 20.4; DB 4; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.23;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGCCGCTTTCTKTRTACNAAGTSGB 25
Db 1 AGCCGCTTTCTTGACAAAGTTGG 25

RESULT 15
PCT-US96-10082A-13
/ Sequence 13, Application PC/TUS9610082A
/ GENERAL INFORMATION:
/ APPLICANT: Life Technologies, Inc.
/ APPLICANT: 8717 Grovemont Circle
/ APPLICANT: Gaithersburg, MD 20884-9980
/ APPLICANT: United States of America
/ APPLICANT: Brasch, Michael A.
/ TITLE OF INVENTION: Recombinational Cloning Using Engineered
/ RECOMBINATION SITES
/ NUMBER OF SEQUENCES: 31
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
/ STREET: 1100 New York Ave., N. W. Suite 600
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3934
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US96/10082A
/ FILING DATE: 07-JUN-1996
/ CLASSIFICATION:
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: both
/ MOLECULE TYPE: cdna
PCT-US96-10082A-13

Query Match      81.6%; Score 20.4; DB 5; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.23;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGCCGCTTTCTKTRTACNAAGTSGB 25
Db 1 AGCCGCTTTCTTGACAAAGTTGG 25

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Job time : 35.9 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:34:49 ; Search time 314 Seconds
(without alignments)
430.015 Million cell updates/sec

Title: US-10-820-133-4

Perfect score: 25

Sequence: 1 agcwgcttcttctacnaagtagb 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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21:	/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21.6	86.4	25	9	US-09-855-797A-4
2	21.6	86.4	25	9	US-09-822-634-5
3	21.6	86.4	25	9	US-09-907-900-4
4	21.6	86.4	25	9	US-09-907-719-4
5	21.6	86.4	25	10	US-09-432-085-4
6	21.6	86.4	25	10	US-09-985-448-4
7	21.6	86.4	25	14	US-10-058-292-4
8	21.6	86.4	25	14	US-10-058-291-4
9	21.6	86.4	25	14	US-10-162-879-4
10	21.6	86.4	25	15	US-10-161-403-4
11	21.6	86.4	25	15	US-10-300-892-4
12	21.6	86.4	25	16	US-10-680-316-4

13	21.6	86.4	25	17	US-10-815-730-4
14	21.6	86.4	25	17	US-10-820-133-4
15	21.6	86.4	25	18	US-10-161-408-36
16	21.6	86.4	25	18	US-10-796-868A-4
17	21.6	86.4	48	17	US-10-250-824-34
18	20.4	81.6	25	9	US-09-855-797A-13
19	20.4	81.6	25	9	US-09-855-797A-40
20	20.4	81.6	25	9	US-09-822-634-10
21	20.4	81.6	25	9	US-09-907-900-13
22	20.4	81.6	25	9	US-09-907-900-40
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25	20.4	81.6	25	10	US-09-432-085-13
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28	20.4	81.6	25	14	US-10-055-001A-8
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30	20.4	81.6	25	14	US-10-058-291-13
31	20.4	81.6	25	14	US-10-162-879-13
32	20.4	81.6	25	15	US-10-161-403-53
33	20.4	81.6	25	15	US-10-300-892-13
34	20.4	81.6	25	15	US-10-300-892-40
35	20.4	81.6	25	16	US-10-680-316-13
36	20.4	81.6	25	16	US-10-680-316-40
37	20.4	81.6	25	17	US-10-815-730-13
38	20.4	81.6	25	17	US-10-815-730-40
39	20.4	81.6	25	17	US-10-820-133-13
40	20.4	81.6	25	17	US-10-820-133-40
41	20.4	81.6	25	18	US-10-161-408-44
42	20.4	81.6	25	18	US-10-796-868A-13
43	20.4	81.6	48	9	US-09-732-914-42
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45	20	80.0	25	9	US-09-732-914-9

ALIGNMENTS

RESULT 1

US-09-855-797A-4
; Sequence 4, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: US 60/065,930
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-4

Query Match 86.4%; Score 21.6; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCWGCCTTTCKTRTACNAAGTSGB 25
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Db 1 AGCCWGCCTTTCKTRTACNAAGTSGB 25

RESULT 2
US-09-822-634-5
; Sequence 5, Application US/09822634
; Patent No. US20020150556A1
; GENERAL INFORMATION:
; APPLICANT: Vile, Richard G.
; APPLICANT: Harrington, Kevin
; APPLICANT: Bateman, Andrew
; APPLICANT: Murphy, Steven
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TISSUE
; TITLE OF INVENTION: SPECIFIC GENE REGULATION THERAPY
; FILE REFERENCE: 07039-289001
; CURRENT APPLICATION NUMBER: US/09/822,634
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/193,977
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated vector sequence
; NAME/KEY: misc.feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: n = A,T,C or G
US-09-822-634-5

Query Match 86.4%; Score 21.6; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCWGCCTTTCKTRTACNAAGTSGB 25
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Db 1 AGCCWGCCTTTCKTRTACNAAGTSGB 25

RESULT 3
US-09-907-900-4
; Sequence 4, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.285004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-4

Query Match 86.4%; Score 21.6; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCWGCCTTTCKTRTACNAAGTSGB 25
|||||
Db 1 AGCCWGCCTTTCKTRTACNAAGTSGB 25

RESULT 4
US-09-907-719-4
; Sequence 4, Application US/09907719
; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-719-4

Query Match 86.4%; Score 21.6; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCWGCCTTTCKTRTACNAAGTSGB 25
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Db 1 AGCCWGCCTTTCKTRTACNAAGTSGB 25

RESULT 5
US-09-432-085-4
; Sequence 4, Application US/09432085
; Publication No. US20030100110A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085


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;
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; Recombination Sites
;
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/058,291
; FILING DATE: 30-Jan-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/432,085
; FILING DATE: 1999-11-02
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
;
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-058-291-4

Query Match 86.4%; Score 21.6; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTCKTRTACNAAGTSG 25
Db 1 AGCCWGCCTTCKTRTACNAAGTSG 25

RESULT 9
US-10-162-879-4
; Sequence 4, Application US/10162879
; Publication No. US2003006879A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; Recombination Sites
;
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/162,879
; FILING DATE: 06-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
;
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-162-879-4

Query Match 86.4%; Score 21.6; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTCKTRTACNAAGTSG 25
Db 1 AGCCWGCCTTCKTRTACNAAGTSG 25

RESULT 10
US-10-161-403-44
; Sequence 44, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: m-attL
; FEATURE:
; NAME/KEY: misc_difference
; LOCATION: 18
; OTHER INFORMATION: n is a o r g o r c o r t/u
US-10-161-403-44

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Query Match 86.4%; Score 21.6; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.4; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

Oy 1 AGCCGCTTTCCTRTACNAAGTSG 25
Db 1 AGCCGCTTTCCTRTACNAAGTSG 25

RESULT 11

US-10-300-892-4
; Sequence 4, Application US/10300892
; Publication No. US20030175970A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/300.892
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-10-300-892-4

Query Match 86.4%; Score 21.6; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.4; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

Oy 1 AGCCGCTTTCCTRTACNAAGTSG 25
Db 1 AGCCGCTTTCCTRTACNAAGTSG 25

RESULT 12

US-10-680-316-4
; Sequence 4, Application US/10680316
; Publication No. US20040063207A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/680.316
; CURRENT FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: US/09/177,387A
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 25

; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-10-680-316-4

Query Match 86.4%; Score 21.6; DB 16; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AGCCGCTTTCCTRTACNAAGTSG 25
Db 1 AGCCGCTTTCCTRTACNAAGTSG 25

RESULT 13

US-10-815-730-4
; Sequence 4, Application US/10815730
; Publication No. US20040171156A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/815.730
; CURRENT FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US/09/177,387A
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-10-815-730-4

Query Match 86.4%; Score 21.6; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.4; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

Oy 1 AGCCGCTTTCCTRTACNAAGTSG 25
Db 1 AGCCGCTTTCCTRTACNAAGTSG 25

RESULT 14

US-10-820-133-4
; Sequence 4, Application US/10820133
; Publication No. US20040171157A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites

```

; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/10/820,133
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US/09/177,387A
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-10-820-133-4

Query Match      86.4%; Score 21.6; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGCCWGCCTTCKTRTACNAAGTSG 25
Db      1 AGCCWGCCTTCKTRTACNAAGTSG 25
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|||||

RESULT 15
US-10-161-408-36
; Sequence 36, Application US/10161408
; Publication No. US20040214290A1
; GENERAL INFORMATION:
; APPLICANT: Perez, Carl
; APPLICANT: Fabijanski, Steven
; APPLICANT: Perkins, Edward
; TITLE OF INVENTION: Plant Artificial Chromosomes, Uses thereof, and Methods of Preparation
; TITLE OF INVENTION: Plant Artificial Chromosomes
; FILE REFERENCE: 24601-419
; CURRENT APPLICATION NUMBER: US/10/161,408
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: US 60/294,687
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: US 60/296,329
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: m-attL recognition sequence
; FEATURE:
; NAME/KEY: misc_difference
; LOCATION: 18
; OTHER INFORMATION: n is a or g or c or t/u
US-10-161-408-36

Query Match      86.4%; Score 21.6; DB 18; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGCCWGCCTTCKTRTACNAAGTSG 25
Db      1 AGCCWGCCTTCKTRTACNAAGTSG 25
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Search completed: November 16, 2004, 11:14:59
Job time : 315.1 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:04 ; Search time 1532 Seconds
(without alignments)
594.643 Million cell updates/sec

Title: US-10-820-133-4

Perfect score: 25
Sequence: 1 agccggcttctktrtaacnaagtsqb 25

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21.6	86.4	1076	7	CK217224 FGAS02922
2	21.6	86.4	1192	7	CK210997 FGAS02282
C 3	20.4	81.6	564	8	BH110378 RPCI-24-3
C 4	20.4	81.6	579	8	BH110594 RPCI-24-3
5	20	80.0	69	7	CF652201 40-L02052
6	20	80.0	79	7	CF651937 24-L02016
C 7	20	80.0	80	6	CB394681 OSTR142B1
8	20	80.0	84	6	CB400948 OSTR185C6
9	20	80.0	87	6	CF652842 80-L02016
10	20	80.0	89	7	CF651862 19-L02052
11	20	80.0	89	7	CF652759 75-L02013
12	20	80.0	89	7	CF653076 94-L02036
13	20	80.0	93	7	CF652843 80-L02016
14	20	80.0	95	7	CF651695 07-L02052
15	20	80.0	95	7	CF651816 16-L02057
16	20	80.0	95	7	CF651859 19-L02036
17	20	80.0	95	7	CF651861 19-L02052
18	20	80.0	95	7	CF651893 21-L02036
19	20	80.0	95	7	CF651957 25-L02036
20	20	80.0	95	7	CF651975 26-L02036
21	20	80.0	95	7	CF652127 35-L02057
22	20	80.0	95	7	CF652128 35-L02057
23	20	80.0	95	7	CF652167 38-L02036
24	20	80.0	95	7	CF652261 44-L02036

25	20	80.0	95	7	CF652333	49-L02013
26	20	80.0	95	7	CF652453	56-L02052
27	20	80.0	95	7	CF652502	59-L02052
28	20	80.0	95	7	CF652546	62-L02036
29	20	80.0	95	7	CF652555	62-L02057
30	20	80.0	95	7	CF652580	64-L02036
31	20	80.0	95	7	CF652581	64-L02036
32	20	80.0	95	7	CF652614	66-L02036
33	20	80.0	95	7	CF652617	66-L02052
34	20	80.0	95	7	CF652673	69-L02058
35	20	80.0	95	7	CF652698	71-L02036
36	20	80.0	95	7	CF652700	71-L02052
37	20	80.0	95	7	CF652763	75-L02035
38	20	80.0	95	7	CF652837	79-L02057
39	20	80.0	95	7	CF652855	80-L02058
40	20	80.0	95	7	CF652890	83-L02013
41	20	80.0	95	7	CF652914	84-L02036
42	20	80.0	95	7	CF652955	86-L02057
43	20	80.0	95	7	CF652980	88-L02052
44	20	80.0	95	7	CF653038	92-L02013
45	20	80.0	95	7	CF653059	93-L02035

ALIGNMENTS

RESULT 1
LOCUS CK217224 1076 bp mRNA linear EST 09-DEC-2003
DEFINITION FGAS029225 Triticum aestivum FGAS: Library 6 CAP GATE 1 Triticum
aestivum CDNA, mRNA sequence.
ACCESSION CK217224
VERSION CK217224.1 GI:396233328
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 1076)
Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,
Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,
Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,
Penniket, C., Roach, J.L. and Sarhan, F.
Functional Genomics of Abiotic Stress in Wheat and Canola Crops
Unpublished (2003)
Contact: Wm L Crosby
Bioinformatics
University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas_est@cs.usask.ca
This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [17,730].
Plate: L68025 row: A column: 06.
Location/Qualifiers
1..1076
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone_lib="Triticum aestivum FGAS: Library 6 CAP GATE 1"
/note="Organ: Crown and leaf; Vector: pCMV.SPORT6; Crown
(50%) and leaf (50%) tissues from wheat cultivar Norstar
after short exposure times to low temperature in the light
and in the dark. 12 mRNA populations were combined before
constructing the library. The first 6 populations: After 7
days of growth at 20C from wheat cultivar Norstar after
short exposure times to low temperature in the light and

in the dark. 12 mRNA populations were combined before constructing the library. The first 6 populations: After 7 days of growth at 20°C, wheat plants were transferred to 4°C in the light. 1cm crown sections and green leaf tissue were separately harvested after 1, 3, and 6 hours of low temperature exposure. The last 6 populations: After 7 days of growth at 20°C, wheat plants were transferred to 4°C in the dark. 1cm crown sections and green leaf tissue were separately harvested after 1, 3, and 6 hours of low temperature exposure. First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with NotI. In addition, this library used a primer for second strand synthesis that annealed to an artificial sequence (RNA oligo) added before first strand synthesis. Therefore when sequences from EST generated from this library will be masked for vector and adaptor sequences, an additional masking step will have to be included to mask this RNA oligo that is common to all clones (sequence CGACTGGAGCAGGACACTGCATGCACTGAGGAGTAGAAA)."

ORIGIN

Query Match 86.4%; Score 21.6; DB 7; Length 1076;
Best Local Similarity 76.0%; Pred. No. 8.2;
Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTCTCTACNAAGTSGB 25
||||:||||:||||:||||:||||:|
Db 760 ACCCAGCTTCTGTACAAAGTGGC 784
||||:||||:||||:||||:||||:|

RESULT 2

CK210997

LOCUS

DEFINITION FGAS022824 Triticum aestivum FGAS: Library 5 GATE 7 Triticum aestivum cDNA, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.

REFERENCE

AUTHORS

1 (bases 1 to 1192)
Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D., Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A., Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D., Penniket, C., Roach, J.L. and Sarhan, F.

Functional Genomics of Abiotic Stress in Wheat and Canola Crops

UNPUBLISHED (2003)

CONTACT: Wm L Crosby

Bioinformatics

University of Saskatchewan, Department of Computer Science

1C101 Engineering Building, 57 Campus Drive, Saskatoon,

Saskatchewan, S7N 5A9, Canada

Tel: 306 966 1769

Fax: 306 966 2033

Email: fgas.ets@cs.usask.ca

This sequence is the direct result of the Base calling software Phred (default parameters). It is the raw base calls. To aid in the identification of the high quality insert the software Lucy (default parameters) has been run on this sequence. Lucy identified the region [125,552].

Plate: L5B024 row: L column: 01.

Location/Qualifiers

1..1192

/organism="Triticum aestivum"

/mol_type="mRNA"

/db_xref="taxon:4565"

/clone_lib="Triticum aestivum FGAS: Library 5 GATE 7"

/note="Vector: pCMV SPORT6; Crown and developmental stages

of spike formation in wheat cultivar Norstar. 4 mRNA

populations were combined before constructing the library. The first mRNA population is from 1cm crown sections after 30 days of cold acclimation. The second is from 1cm crown sections after 11 days of deacclimation (before deacclimation plants were fully vernalized for 49 days). The third is from different developmental stages of spike formation (5 to 50mm) that still have not emerged from the leaf (dissection required). The last is from different developmental stages of spike and seed formation after having emerged from the leaf (visible). First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with NotI."

ORIGIN

Query Match 86.4%; Score 21.6; DB 7; Length 1192;
Best Local Similarity 76.0%; Pred. No. 8.4;
Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTCTCTACNAAGTSGB 25
||||:||||:||||:||||:||||:|
Db 650 AGCCAGCTTCTGTACAAAGTGGT 674
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RESULT 3

BH110378/c

LOCUS

DEFINITION RPCI-24-367J19.TJ RPCI-24 Mus musculus genomic clone
RPCI-24-367J19, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 564)

Tsagayev, G., Geer, K., Krol, M., Shvartsbeyn, A., Akimret, B., Levins, M., Russell, D., de Jong, P. and Fraser, C.M.

Mouse BAC End sequences from Library RPCI-24

Unpublished (1999)

Other GSSs: RPCI-24-367J19.TV

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-24. For BAC

library availability, please contact Pieter de Jong

pdejong@mail.cho.org. Clones may be purchased from BACPAC

Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC endPage: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Plate: 367 row: J column: 19

Seq primer: SP6

Class: BAC ends.

Location/Qualifiers

1..564

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-24-367J19"

/sex="Male"

/cell_type="Spleen/Brain"

/clone_lib="RPCI-24"

/note="Vector: pTARBAC1; Site 1: BamHI; Site 2: BamHI;

RPCI-24 Mouse BAC Library produced by Pieter de Jong. The

library was cloned in the pTARBAC1 cloning vector at the

BamHI sites using MboI partially digested male C57BL/6J

DNA."

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ORIGIN
Query Match      81.6%; Score 20.4; DB 8; Length 564;
Best Local Similarity 76.0%; Pred. No. 30;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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RESULT 4
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DEFINITION
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  RPCI-24-367L19.TJ RPCI-24 Mus musculus genomic clone
  RPCI-24-367L19, genomic survey sequence.
ACCESSION
  BH110594
VERSION
  BH110594.1 GI:14944870
KEYWORDS
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SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 579)
AUTHORS
  Zhao,S., Niemman,M., Malek,J., Shatsman,S., Alkinret,B., Levins,M.,
  Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregorgis,B.,
  Russell,D., de Jong,P. and Fraser,C.M.
  Mouse BAC End Sequences from Library RPCI-24
  Unpublished (1999)
JOURNAL
  Other GSSs: RPCI-24-367L19.TV
COMMENT
  Contact: Shaying Zhao
  Department of Eukaryotic Genomics
  The Institute for Genomic Research
  9712 Medical Center Dr., Rockville, MD 20850, USA
  Tel: 301 838 0200
  Fax: 301 838 0208
  Email: szhaotigr.org
  Clones are derived from the mouse BAC library RPCI-24. For BAC
  library availability, please contact Pieter de Jong
  (pdejong@mail.cho.org). Clones may be purchased from BACPAC
  Resources (http://www.choi.org/bacpac/orderingframe.html). BAC end
  page: http://www.tigr.org/tdb/bac\_ends/mouse/bac\_end\_intro.html
  Plate: 367 row: L column: 19
  Seq primer: SP6
  Class: BAC ends.
FEATURES
  source
  Location/Qualifiers
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    DNA."
ORIGIN
Query Match      81.6%; Score 20.4; DB 8; Length 579;
Best Local Similarity 76.0%; Pred. No. 30;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCCGCTTCTCTACNAAGTSGB 25
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CF652201
LOCUS
DEFINITION
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  24-L020167-066-001-P06-SP6P MP12-ADIS-066 Arabidopsis thaliana cDNA
  clone MP12p2001P061Q 5-PRIME, mRNA sequence.
ACCESSION
  CF652201
VERSION
  CF652201.1 GI:37428467
KEYWORDS
  EST.
SOURCE
  Arabidopsis thaliana (thale cress)
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE
  1 (bases 1 to 69)
AUTHORS
  Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T.,
  Mitchell-Olds,T. and Weissenhaar,B.
  Large-scale identification and analysis of genome-wide
  single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
  Genome Res. 13 (6), 1250-1257 (2003)
JOURNAL
  22683290
MEDLINE
  12799357
PUBMED
  Contact: Weissenhaar B
  ADIS DNA core facility at MP12
  Max-Planck-Institute for Plant Breeding Research
  Carl-von-Linne Weg 10, 50829 Koeln, Germany
  Fax: 00492215062851
  Email: weissenhaa@mpiz-koeln.mpg.de
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  Location/Qualifiers
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    /clone="MP12p2001P093Q"
    /tissue_type="root"
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    Wasselewskija-0; roots from three weeks old plants grown
    on MS-plates at 26M-OC with 16 hours light/day; library
    was made at the Max-Planck-Institute for Plant Breeding
    Research, Cologne, Germany; cloning sites SalI-NotI,
    primer sites and orientation:
    SP6-Sali-CCAGCGTCGC-5prime-cDNA-polyA-CC-NotI-T7; GATEWAY
    compatible; Note: Sequencing granted in the context of the
    GABI Arabidopsis Verbund I: Genetic Diversity,
    'Establishment of high-efficiency SNP-based mapping tools
    and development of methods for genome-wide mutation
    detection', PI: Bernd Weissenhaar Sequence submission managed
    by RZPD/GABI-Primary database: http://gabi.rzpd.de This
    clone is available from RZPD; contact RZPD (clone@rzpd.de)
    for further information."
ORIGIN
Query Match      80.0%; Score 20; DB 7; Length 69;
Best Local Similarity 72.0%; Pred. No. 31;
Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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RESULT 6
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LOCUS
DEFINITION
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ACCESSION
  CF651937
VERSION
  CF651937.1 GI:37427952

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KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi;
1 (bases 1 to 79)
REFERENCE
AUTHORS
Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T.,
Mitchell-Olds,T. and Weissshaar,B.
TITLE
Large-scale identification and analysis of genome-wide
single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
JOURNAL
MEDLINE
12683290
PUBMED
1279357
COMMENT
Contact: Weissshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissshaar@mpiz-koeln.mpg.de
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Seq primer: SP6P; Location/Qualifiers
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/lab_host="E. coli TOP10"
/clone_lib="MP12-ADIS-066"
/notes="Vector: PCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from Arabidopsis thaliana, accession
Wassilewskija-0; roots from three weeks old plants grown
on WS-plates at 26M-OC with 16 hours light/day; library
was made at the Max-Planck-Institute for Plant Breeding
Research, Cologne, Germany; cloning sites SalI-NotI,
Primer sites and orientation:
SP6-SalI-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; GATEWAY
compatible; Note: Sequencing granted in the context of the
GABI Arabidopsis Verbund I: Genetic Diversity,
'Establishment of high-efficiency SNP-based mapping tools
and development of methods for genome-wide mutation
detection' PI: Bernd Weissshaar Sequence submission managed
by RZPD/GABI-Primary database: http://gabi.rzpd.de This
clone is available from RZPD; contact RZPD (clone@rzpd.de)
for further information."

ORIGIN
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Best Local Similarity 72.0%; Pred. No. 32;
Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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Db 48 ACCCAGCTTCTTGTCACAAAGTGGT 72

RESULT 7
CB394681/c
LOCUS
CB394681
DEFINITION
OSTR142B12_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION
CB394681
VERSION
CB394681.1 GI:30736392
KEYWORDS
EST.
SOURCE
Caenorhabditis elegans
ORGANISM
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 80)
REFERENCE
AUTHORS
Nat. Genet. (2003) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute

AUTHORS
Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M.,
Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T.,
Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevet,E., Papasotiriopoulos,V.,
Tolias,P.P., Placek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.
TITLE
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
JOURNAL
Nat. Genet. (2003) In press
COMMENT
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@fci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@fci.harvard.edu or
marc_vidal@fci.harvard.edu
POLYA-No. Location/Qualifiers
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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"

ORIGIN
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Best Local Similarity 72.0%; Pred. No. 32;
Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTCTKTRTACNAAAGTSGB 25
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Db 55 ACCCAGCTTCTTGTCACAAAGTGGT 31

RESULT 8
CB400948
LOCUS
CB400948
DEFINITION
OSTF185C6_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION
CB400948
VERSION
CB400948.1 GI:30742675
KEYWORDS
EST.
SOURCE
Caenorhabditis elegans
ORGANISM
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 84)
REFERENCE
AUTHORS
Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M.,
Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T.,
Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevet,E., Papasotiriopoulos,V.,
Tolias,P.P., Placek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.
TITLE
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
JOURNAL
Nat. Genet. (2003) In press
COMMENT
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute

```

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu

POLYA=No.

FEATURES

source Location/Qualifiers

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ORIGIN

Query Match 80.0%; Score 20; DB 6; Length 84;

Best Local Similarity 72.0%; Pred. No. 33;

Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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Db 35 ACCCAGCTTCTTGTACAAAGTGGG 59

RESULT 9

CF652842

LOCUS

80-L020166-066-001-P19-SP6P MP12-ADIS-066 Arabidopsis thaliana cDNA

clone MP12p2001P19Q 5-PRIME, mRNA sequence.

CF652842

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

1 (bases 1 to 87)

Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T.,

Mitchell-Olds,T. and Weisshaar,B.

Large-scale identification and analysis of genome-wide

single-nucleotide polymorphisms for mapping in Arabidopsis thaliana

Genome Res. 13 (6), 1250-1257 (2003)

22683290

PUBMED

12799357

COMMENT

Contact: Weisshaar B

ADIS DNA core facility at MP12

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

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Seq primer: SP6P;

Location/Qualifiers

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/note="vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;

cDNA library from Arabidopsis thaliana, accession

Wassilewskaja-0; roots from three weeks old plants grown

on MS-plates at 26M-OC with 16 hours light/day; library

was made at the Max-Planck-Institute for Plant Breeding

Research, Cologne, Germany; Cloning sites SalI-NotI,

primer sites and orientation:

SP6-Sali-CCAGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; GATEWAY

compatible; Note: Sequencing granted in the context of the

GABI Arabidopsis Verbund I: Genetic Diversity,

'Establishment of high-efficiency SNP-based mapping tools

and development of methods for genome-wide mutation

detection'; PI: Bernd Weisshaar Sequence submission managed

by RZPD/GABI-Primary database: <http://gabi.rzpd.de> This

clone is available from RZPD; contact RZPD (clone@rzpd.de)

for further information."

ORIGIN

Query Match 80.0%; Score 20; DB 7; Length 87;

Best Local Similarity 72.0%; Pred. No. 33;

Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCCWGCCTTCTKTRTACNAAGTSG 25

Db 44 ACCCAGCTTCTTGTACAAAGTGGT 68

RESULT 10

CF651862

LOCUS

19-L02024-066-003-E06-SP6P MP12-ADIS-066 Arabidopsis thaliana cDNA

clone MP12p2001E063Q 5-PRIME, mRNA sequence.

CF651862

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

1 (bases 1 to 89)

Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T.,

Mitchell-Olds,T. and Weisshaar,B.

Large-scale identification and analysis of genome-wide

single-nucleotide polymorphisms for mapping in Arabidopsis thaliana

Genome Res. 13 (6), 1250-1257 (2003)

22683290

PUBMED

12799357

COMMENT

Contact: Weisshaar B

ADIS DNA core facility at MP12

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

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Location/Qualifiers

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/note="vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;

cDNA library from Arabidopsis thaliana, accession

detection' PI: Bernd Weisshaar Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de> This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further information."

ORIGIN

Query Match 80.0%; Score 20; DB 7; Length 89;
Best Local Similarity 72.0%; Pred. No. 33;
Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCCGCTTTCTKTRTACNAAGTSG 25

Db 44 ACCGAGCTTTCTGTACAAAGTGT 68

RESULT 13

CF652843

LOCUS

DEFINITION 80-L020167-066-001-P20-SP6P MP1Z-ADIS-066 Arabidopsis thaliana CDNA clone MP1Zp2001P201Q 5-PRIME, mRNA sequence.

ACCESSION CF652843

VERSION CF652843.1

KEYWORDS EST.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 93)

AUTHORS Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T., Mitchell-Olds,T. and Weisshaar,B.

TITLE Large-scale identification and analysis of genome-wide

JOURNAL single-nucleotide polymorphisms for mapping in Arabidopsis thaliana

MEDLINE Genome Res. 13 (6), 1250-1257 (2003)

PUBMED 22683290

COMMENT 12799357

Contact: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

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Seq primer: SP6P.

Location/Qualifiers

1..93

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/tissue_type="root"

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/clone_lib="MP1Z-ADIS-066"

/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;

cDNA library from Arabidopsis thaliana, accession

Wasilewskja-0; roots from three weeks old plants grown

on MS-plates at 26M-OC with 16 hours light/day; library

was made at the Max-Planck-Institute for Plant Breeding

Research, Cologne, Germany; cloning sites SalI-NotI,

primer sites and orientation:

SP6-SalI-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; GATEWAY

compatible; Note: Sequencing granted in the context of the

GABI Arabidopsis Verbund I: Genetic Diversity,

'Establishment of high-efficiency SNP-based mapping tools

and development of methods for genome-wide mutation

detection' PI: Bernd Weisshaar Sequence submission managed

by RZPD/GABI-Primary database: <http://gabi.rzpd.de> This

clone is available from RZPD; contact RZPD (clone@rzpd.de)

for further information."

ORIGIN

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Best Local Similarity 72.0%; Pred. No. 33;
Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Query Match

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Best Local Similarity 72.0%; Pred. No. 33;
Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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1 AGCCGCTTTCTKTRTACNAAGTSG 25

Db

50 ACCGAGCTTTCTGTACAAAGTGT 74

RESULT 14

CF651695

LOCUS

DEFINITION 07-L020525-066-003-N01-SP6P MP1Z-ADIS-066 Arabidopsis thaliana CDNA clone MP1Zp2001N013Q 5-PRIME, mRNA sequence.

ACCESSION CF651695

VERSION CF651695.1

KEYWORDS EST.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 95)

AUTHORS Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T., Mitchell-Olds,T. and Weisshaar,B.

TITLE Large-scale identification and analysis of genome-wide

JOURNAL single-nucleotide polymorphisms for mapping in Arabidopsis thaliana

MEDLINE Genome Res. 13 (6), 1250-1257 (2003)

PUBMED 22683290

COMMENT 12799357

Contact: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

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Seq primer: SP6P.

Location/Qualifiers

1..95

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/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;

cDNA library from Arabidopsis thaliana, accession

Wasilewskja-0; roots from three weeks old plants grown

on MS-plates at 26M-OC with 16 hours light/day; library

was made at the Max-Planck-Institute for Plant Breeding

Research, Cologne, Germany; cloning sites SalI-NotI,

primer sites and orientation:

SP6-SalI-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; GATEWAY

compatible; Note: Sequencing granted in the context of the

GABI Arabidopsis Verbund I: Genetic Diversity,

'Establishment of high-efficiency SNP-based mapping tools

and development of methods for genome-wide mutation

detection' PI: Bernd Weisshaar Sequence submission managed

by RZPD/GABI-Primary database: <http://gabi.rzpd.de> This

clone is available from RZPD; contact RZPD (clone@rzpd.de)

for further information."

ORIGIN

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:29:43.; Search time 708.5 Seconds
(without alignments)
1668.656 Million cell updates/sec

Title: US-10-820-133-5

Perfect score: 25

Sequence: 1 gttcagcttktttacnaagtsb 25

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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3	21.6	86.4	25	6	ARI493777 Sequence
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5	21.6	86.4	25	6	AX498615 Sequence
6	21.6	86.4	25	6	AX787513 Sequence
7	21.6	86.4	25	6	BD131331 Recombina
8	21.6	86.4	25	6	BD131337 Recombina
9	21.6	86.4	37	6	CQ758822 Sequence
10	21.6	86.4	102	6	BD263460 Compositi
11	21.6	86.4	102	6	BD263462 Compositi
12	21.6	86.4	135	6	BD263228 Compositi
13	21.6	86.4	153	6	BD263458 Compositi
14	21.6	86.4	204	6	BD263433 Compositi
15	21.6	86.4	255	6	BD263435 Compositi
16	21.6	86.4	1846	6	AX703501 Sequence
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28	21.6	86.4	6422	6	BD263362 Compositi
29	21.6	86.4	6464	6	BD263349 Compositi
30	21.6	86.4	6526	6	BD263356 Compositi
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39	21.6	86.4	6964	6	BD263352 Compositi
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ACCESSION ARI24525
VERSION ARI24525.1 GI:14109886
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6171861-A 5 09-JAN-2001;
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LOCUS
DEFINITION Sequence 5 from patent US 6270969.
ACCESSION ARI63176
VERSION ARI63176.1 GI:16233684
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites

JOURNAL Patent: US 6270969-A 5 07-AUG-2001;
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LOCUS
DEFINITION Sequence 5 from patent US 6720140.
ACCESSION AR493777
VERSION AR493777.1 GI:47266190
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6720140-A 5 13-APR-2004;
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RESULT 4
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LOCUS
DEFINITION Sequence 5 from Patent EP1227147.
ACCESSION AX491644
VERSION AX491644.1 GI:22324152
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE
1
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1227147-A 5 31-JUL-2002;
INVITROGEN CORPORATION (US)
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JOURNAL Patent: US 6270969-A 5 07-AUG-2001;
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LOCUS
DEFINITION Sequence 5 from Patent EP1229113.
ACCESSION AX498615
VERSION AX498615.1 GI:23343412
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE
1
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1229113-A 5 07-AUG-2002;
INVITROGEN CORPORATION (US)
FEATURES Location/Qualifiers
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RESULT 6
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DEFINITION Sequence 30 from Patent WO03044207.
ACCESSION AX787513
VERSION AX787513.1 GI:32954587
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE
1
AUTHORS Nomura,N., Goshima,N., Kieu,Y. and Sono,S.
TITLE Method for the preparation of nucleic acids
JOURNAL Patent: WO 03044207-A 30 30-MAY-2003;
Invitrogen Japan K.K. (JP) ; National Institute of Advanced
Industrial Science and Technology (JP)
FEATURES Location/Qualifiers
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RESULT 7
BD131331
LOCUS
DEFINITION Recombinational cloning using nucleic acids having recombination
sites.
ACCESSION BD131331

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VERSION      BD131331.1  GI:23226276
KEYWORDS     JP 2002500861-A/5.
SOURCE       unidentified
ORGANISM     unclassified.
REFERENCE    1 (bases 1 to 25)
AUTHORS     Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE       Recombinational cloning using nucleic acids having recombination
JOURNAL     Patent: JP 2002500861-A 5 15-JAN-2002;
COMMENT     LIFE TECHNOLOGIES INC
OS          Unknown
PN          JP 2002500861-A/5
PD          15-JAN-2002
PF          26-OCT-1998  JP 2000518069
PR          24-OCT-1997  US  60/065930,23-OCT-1998  US  09/177387 PI
JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DONNA K FOX PC
C12N15/09,C12Q1/68,C12N15/00
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Key         Location/Qualifiers
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RESULT 8
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DEFINITION Recombinational cloning using nucleic acids having recombination
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ACCESSION   BD131337
VERSION     BD131337.1  GI:23226282
KEYWORDS    JP 2002500861-A/11.
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 25)
AUTHORS     Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE       Recombinational cloning using nucleic acids having recombination
JOURNAL     Patent: JP 2002500861-A 11 15-JAN-2002;
COMMENT     LIFE TECHNOLOGIES INC
OS          Unknown
PN          JP 2002500861-A/11
PD          15-JAN-2002
PF          26-OCT-1998  JP 2000518069
PR          24-OCT-1997  US  60/065930,23-OCT-1998  US  09/177387 PI
JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DONNA K FOX PC
C12N15/09,C12Q1/68,C12N15/00
CC          Description of Unknown Organism: recombination products FH
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RESULT 9
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LOCUS       BD131337              25 bp    DNA    linear    PAT 17-JUL-2003
DEFINITION Compositions and methods for use in recombinational cloning of
            nucleic acids.
ACCESSION   BD263460
VERSION     BD263460.1  GI:33073228
KEYWORDS    JP 2002537790-A/238.
SOURCE      synthetic construct
ORGANISM     artificial sequences.
REFERENCE   1 (bases 1 to 102)
AUTHORS     Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
TITLE       Compositions and methods for use in recombinational cloning of
            nucleic acids
JOURNAL     Patent: JP 2002537790-A 238 12-NOV-2002;
COMMENT     INVITROGEN CORP
OS          Artificial Sequence
PN          JP 2002537790-A/238
PD          12-NOV-2002
PF          02-MAR-2000  JP 2000602252
PR          02-MAR-1999  US  60/122389,23-MAR-1999  US  60/126049 PR
28-MAY-1999  US  60/136744
PI          JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DAVID CHEO PC
C12N15/09,C07K14/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/10
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Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

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LOCUS       BD131337              37 bp    DNA    linear    PAT 01-MAR-2004
DEFINITION Sequence 13 from Patent WO2003106691.
ACCESSION   CQ758822
VERSION     CQ758822.1  GI:44848843
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM     artificial sequences.
REFERENCE   1
AUTHORS     Boesten,W.H., Raemakers-Franken,P.C., Sonke,T., Euverink,G.J. and
            Grijpsma,P.
TITLE       POLYPEPTIDES HAVING H-AMINO ACID AMIDE RACEMASE ACTIVITY AND
            NUCLEIC ACIDS ENCODING THE SAME
JOURNAL     Patent: WO 2003106691-A 13 24-DEC-2003;
            DSM IP Assets B.V. (NL)
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Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

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Db 37 GTTCAGCTTTTKTRTACNAAGTSGT 13

RESULT 10
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LOCUS       BD263460              102 bp   DNA    linear    PAT 17-JUL-2003
DEFINITION Compositions and methods for use in recombinational cloning of
            nucleic acids.
ACCESSION   BD263460
VERSION     BD263460.1  GI:33073228
KEYWORDS    JP 2002537790-A/238.
SOURCE      synthetic construct
ORGANISM     artificial sequences.
REFERENCE   1 (bases 1 to 102)
AUTHORS     Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
TITLE       Compositions and methods for use in recombinational cloning of
            nucleic acids
JOURNAL     Patent: JP 2002537790-A 238 12-NOV-2002;
COMMENT     INVITROGEN CORP
OS          Artificial Sequence
PN          JP 2002537790-A/238
PD          12-NOV-2002
PF          02-MAR-2000  JP 2000602252
PR          02-MAR-1999  US  60/122389,23-MAR-1999  US  60/126049 PR
28-MAY-1999  US  60/136744
PI          JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DAVID CHEO PC
C12N15/09,C07K14/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/10
CC          CDS
Key         Location/Qualifiers
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DEFINITION Compositions and methods for use in recombinational cloning of
            nucleic acids.
ACCESSION BD263433
VERSION   BD263433.1 GI:33073201
KEYWORDS  JP 2002537790-A/211.
SOURCE    synthetic construct
ORGANISM  artificial sequences.
REFERENCE 1 (bases 1 to 204)
AUTHORS   Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
TITLE     Compositions and methods for use in recombinational cloning of
            nucleic acids
JOURNAL   Patent: JP 2002537790-A 211 12-NOV-2002;
COMMENT   INVITROGEN CORP
          PN JP 2002537790-A/211
          PD 12-NOV-2002
          PF 02-MAR-2000 JP 2000602252
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          28-MAY-1999 US 60/136744
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RESULT 15
BD263435
LOCUS     255 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Compositions and methods for use in recombinational cloning of
            nucleic acids.
ACCESSION BD263435
VERSION   BD263435.1 GI:33073203
KEYWORDS  JP 2002537790-A/213.
SOURCE    synthetic construct
ORGANISM  artificial sequences.
REFERENCE 1 (bases 1 to 255)
AUTHORS   Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
TITLE     Compositions and methods for use in recombinational cloning of
            nucleic acids
JOURNAL   Patent: JP 2002537790-A 213 12-NOV-2002;
COMMENT   INVITROGEN CORP
          PN JP 2002537790-A/213
          PD 12-NOV-2002
          PF 02-MAR-2000 JP 2000602252
          PR 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR
          28-MAY-1999 US 60/136744
          PT JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DAVID CHEO PC
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C12N15/09,C07K14/00,C12N1/15,C12N1/19,C12N5/10,C12N15/10,C12N15/10,
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
782.095 Million cell updates/sec

Title: US-10-820-133-5

Perfect score: 25

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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8	21.6	86.4	25	8	ABT16625
9	21.6	86.4	25	9	ACD28280
10	21.6	86.4	25	9	ACD28480
11	21.6	86.4	25	9	ADA38166
12	21.6	86.4	25	10	AAD60562
13	21.6	86.4	25	10	ABZ58738
14	21.6	86.4	25	10	ACC59582
15	21.6	86.4	25	10	ACCA4654
16	21.6	86.4	25	12	ADJ46356
17	21.6	86.4	25	12	ADL93420
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ALIGNMENTS

RESULT 1

AAT48214

ID AAT48214 standard; DNA; 25 BP.

XX AC AAT48214;

DT 20-OCT-1997 (first entry)

XX DE M-attp1 core region.

XX KW att recombination site; core region; mutation; enhance; recombination;

XX OS Synthetic.

XX FN WO9640724-A1.

XX PD 19-DEC-1996.

XX PF 07-JUN-1996; 96WO-US010082.

XX PR 07-JUN-1995; 95US-00486139.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX FI Hartley JL, Brasch MA;

XX DR WPI, 1997-065168/06.

XX PT Nucleic acids, vectors and methods to obtain chimeric nucleic acid -

XX PT using recombinant proteins and engineered recombination sites in vitro or

XX PS Claim 14; Page 55; 106pp; English.

XX CC AAT48210-25 are att recombination site core region DNA sequences. The

XX CC core region has at least one engineered mutation that enhances

XX CC recombination in vitro in the formation of a Cointegrate or Product DNA.

XX CC These core regions can be incorporated into novel vector donor DNA

XX CC molecules. The nucleic acids, vectors and methods of the invention are

XX CC used to obtain chimeric nucleic acid using recombination proteins and

XX CC engineered recombination sites in vitro or in vivo. The improved

XX CC specificity, speed and yields of the invention facilitates DNA or RNA

XX CC subcloning, regulation or exchange useful for any related purpose, e.g.

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30 21.6 86.4 5148 6 AAD27063
31 21.6 86.4 5375 12 ADI34682
32 21.6 86.4 5558 12 ADI90419
33 21.6 86.4 5692 12 ADQ48540
34 21.6 86.4 5763 12 ADQ48544
35 21.6 86.4 5848 3 AAC55481
36 21.6 86.4 5957 3 AAC55467
37 21.6 86.4 6025 3 AAC55469
38 21.6 86.4 6025 3 AAC55507
39 21.6 86.4 6264 3 AAC55491
40 21.6 86.4 6354 3 AAC55483
41 21.6 86.4 6422 3 AAC55454
42 21.6 86.4 6464 10 ABZ58765
43 21.6 86.4 6526 3 AAC55471
44 21.6 86.4 6553 3 AAC55456
45 21.6 86.4 6553 3 AAC55456

CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
 CC or modification of transcribed, replicated, isolated or genomic DNA or
 CC RNA

SQ Sequence 25 BP; 4 A; 3 C; 4 G; 8 T; 0 U; 6 Other;
 Query Match 86.4%; Score 21.6; DB 2; Length 25;
 Best Local Similarity 100.0%; Pred. NO. 2.2;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTYYKTRTACNAAGTSG 25
 Db 1 GTTCAGCTTYYKTRTACNAAGTSG 25

RESULT 2

AAx78945
 ID AAX78945 standard; DNA; 25 BP.

XX AC AAX78945;

DT 17-AUG-1999 (first entry)

DE Oligonucleotide #11 for recombination and cloning method.

XX Cloning; donor; recombination site; vector; chimeric; ss.

OS Synthetic.

PN WO9921977-A1.

XX 06-MAY-1999.

PF 26-OCT-1998; 98WO-US022589.

PR 24-OCT-1997; 97US-0065930P.

XX 23-OCT-1998; 98US-00177387.

PA (LIFE-) LIFE TECHNOLOGIES INC.

PI Hartley JL, Brasch MA, Temple GF, Fox DK;

DR WPI; 1999-303011/25.

XX New nucleic acid cloning methods.

PS Disclosure; Page 161; 185pp; English.

CC The invention relates to novel methods for cloning or subcloning one or
 CC more nucleic acid molecules (NAMES) comprising: (a) combining in vitro or
 CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
 CC more desired nucleic acid segments flanked by at least 2 recombination
 CC sites which do not recombine with each other; (2) one or more vector
 CC donor molecules (VDMs) comprising at least 2 recombination sites which do
 CC not recombine with each other; and (3) one or more site-specific
 CC recombination proteins; (b) incubating the combination to transfer one or
 CC more of the desired segments into one or more of the VDMs, thereby
 CC producing one or more desired product molecules (PMs). The methods can be
 CC used for the efficient and specific recombination of NAM segments. They
 CC can be used to generate chimeric DNA or RNA molecules that have the
 CC desired characteristics and/or nucleic acid segments. The methods can
 CC also be used for changing vectors. The oligonucleotides AAX78935-X78994
 CC are used in the method of the invention

SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 U; 0 Other;

Query Match 86.4%; Score 21.6; DB 2; Length 25;
 Best Local Similarity 76.0%; Pred. NO. 2.2;
 Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTYYKTRTACNAAGTSG 25

Db 1 GTTCAGCTTCTTGTACAAAGTGGT 25

RESULT 3

AAx78939
 ID AAX78939 standard; DNA; 25 BP.

XX AC AAX78939;

DT 17-AUG-1999 (first entry)

DE Oligonucleotide #5 for recombination and cloning method.

XX Cloning; donor; recombination site; vector; chimeric; ss.

OS Synthetic.

PN WO9921977-A1.

XX 06-MAY-1999.

PF 26-OCT-1998; 98WO-US022589.

PR 24-OCT-1997; 97US-0065930P.

XX 23-OCT-1998; 98US-00177387.

PA (LIFE-) LIFE TECHNOLOGIES INC.

PI Hartley JL, Brasch MA, Temple GF, Fox DK;

DR WPI; 1999-303011/25.

XX New nucleic acid cloning methods.

PS Disclosure; Page 159; 185pp; English.

CC The invention relates to novel methods for cloning or subcloning one or
 CC more nucleic acid molecules (NAMES) comprising: (a) combining in vitro or
 CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
 CC more desired nucleic acid segments flanked by at least 2 recombination
 CC sites which do not recombine with each other; (2) one or more vector
 CC donor molecules (VDMs) comprising at least 2 recombination sites which do
 CC not recombine with each other; and (3) one or more site-specific
 CC recombination proteins; (b) incubating the combination to transfer one or
 CC more of the desired segments into one or more of the VDMs, thereby
 CC producing one or more desired product molecules (PMs). The methods can be
 CC used for the efficient and specific recombination of NAM segments. They
 CC can be used to generate chimeric DNA or RNA molecules that have the
 CC desired characteristics and/or nucleic acid segments. The methods can
 CC also be used for changing vectors. The oligonucleotides AAX78935-X78994
 CC are used in the method of the invention

SQ Sequence 25 BP; 4 A; 3 C; 4 G; 8 T; 0 U; 6 Other;

Query Match 86.4%; Score 21.6; DB 2; Length 25;
 Best Local Similarity 100.0%; Pred. NO. 2.2;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTYYKTRTACNAAGTSG 25

Db 1 GTTCAGCTTYYKTRTACNAAGTSG 25

RESULT 4

AAx06185
 ID AAS06185 standard; DNA; 25 BP.

XX AC AAS06185;

DT 12-SEP-2001 (first entry)

DE Phage-lambda recombination site attR2.

XX Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;

```

KW lambda integrase; therapeutic; ss.
OS Bacteriophage lambda.
XX WO200142509-A1.
XX 14-JUN-2001.
XX 11-DEC-2000; 2000WO-US033546.
XX 10-DEC-1999; 99US-0169983P.
XX 09-MAR-2000; 2000US-0188020P.
XX (CHEO/) CHEO D.
XX (BRAS/) BRASCH M A.
XX (TEMP/) TEMPLE G F.
XX (HART/) HARTLEY J L.
XX (BYRD/) BYRD D R N.
XX Cheo D, Brasch MA, Temple GF, Hartley JL, Byrd DRN;
XX WPI; 2001-356174/37.
XX Producing hybrid nucleic acids, useful for expressing novel therapeutic
XX polypeptides, by mixing the same or different nucleic acids having one or
XX more recombination sites in the presence of recombination proteins, e.g.
XX Cre.
XX Disclosure; Fig 24A; 357pp; English.
XX AAS06174-AAS06322 represent Bacteriophage lambda att recombination site
XX nucleic acid sequences, and PCR primers of the invention. The att
XX sequences are recognised by the recombination protein lambda integrase
XX (Int). The invention is a new method of producing a population of hybrid
XX nucleic acids comprising mixing at least a first population of nucleic
XX acids comprising one or more recombination sites with at least one target
XX nucleic acid comprising one or more recombination sites and causing some
XX or all of the nucleic acids to recombine with all or some of the target
XX nucleic acids. The method is useful for producing a population of hybrid
XX nucleic acids which may be the same or different. The nucleic acids may
XX be used to express therapeutic proteins or peptides and they may also be
XX used to create novel fusion proteins by expressing different sequences
XX linked to each other. The method allows simultaneous cloning of two or
XX more different nucleic acids
XX Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 U; 0 Other;
XX
XX Query Match 86.4%; Score 21.6; DB 4; Length 25;
XX Best Local Similarity 76.0%; Pred. NO. 2.2;
XX Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 1 GTTCAGCTTTTKTRTACNAAGTSGB 25
XX |||||:::|||||
XX Db 1 GTTCAGCTTTCTGTACAAAGTGGT 25
XX
XX RESULT 5
XX AAC87870
XX ID AAC87870 standard; DNA; 25 BP.
XX AC AAC87870;
XX XX
XX DT 02-MAR-2001 (first entry)
XX DE Escherichia coli core region recombinant site m-attP1 SEQ ID NO:5.
XX XX Core region; recombination site; cloning; chimeric DNA; characteristic;
XX KW mutation; att site; lox site; ss.
XX OS Escherichia coli.
XX XX US6143557-A.
XX PN
XX XX

PD 07-NOV-2000.
XX 20-JAN-1999; 99US-00233493.
XX 07-JUN-1995; 95US-00486139.
XX 07-JUN-1996; 96US-00663002.
XX 12-JAN-1998; 98US-00005476.
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX Brasch MA, Hartley JL;
XX WPI; 2001-049004/06.
XX Isolated nucleic acid molecules comprising a DNA segment having two
XX engineered recombination sites, derived from att or lox, which flank a
XX selectable marker and comprise a core region having an engineered
XX mutation.
XX Claim 1; Col 18; 73pp; English.
XX The present invention describes an isolated nucleic acid molecule (I)
XX comprising a first nucleic acid sequence having a defined sequence
XX (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,
XX or an RNA sequence corresponding to AAC87866 to AAC87881. Also described
XX are: (1) an isolated nucleic acid molecule (II) comprising a first
XX mutated recombination site that removes one or more stop codons from the
XX recombination site or avoids hairpin formation, the recombination site
XX being an att or lox site; (2) an isolated nucleic acid molecule (III)
XX comprising a first att recombination site comprising a mutation that
XX enhances recombination specificity; (3) vectors (IV) comprising the above
XX mentioned nucleic acids; and (4) cells comprising the above mentioned
XX nucleic acids or (IV). The nucleic acids are used in engineering a core
XX region of a given recombination site to provide mutative sites suitable
XX for subcloning reactions. The use of nucleic acids for obtaining
XX engineered recombination in vitro or in vivo makes the methods for DNA or
XX RNA subcloning, highly specific, rapid, and less labour intensive
XX
XX Sequence 25 BP; 4 A; 3 C; 4 G; 8 T; 0 U; 6 Other;
XX
XX Query Match 86.4%; Score 21.6; DB 4; Length 25;
XX Best Local Similarity 100.0%; Pred. No. 2.2;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 GTTCAGCTTTTKTRTACNAAGTSGB 25
XX |||||:::|||||
XX Db 1 GTTCAGCTTTTKTRTACNAAGTSGB 25
XX
XX RESULT 6
XX AAF55739
XX ID AAF55739 standard; DNA; 25 BP.
XX XX
XX AC AAF55739;
XX XX
XX DT 12-APR-2001 (first entry)
XX DE Recombination site m-attP1.
XX XX Recombination site; cloning; m-att; ss.
XX OS Unidentified.
XX PN US6171861-B1.
XX XX
XX PD 09-JAN-2001.
XX PF 12-JAN-1998; 98US-00005476.
XX PR 07-JUN-1995; 95US-00486139.
XX PR 07-JUN-1996; 96US-00663002.
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX PA

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XX
PI Hartley JL, Brasch MA;
XX WPI; 2001-136877/14.
DR
XX
PT In vitro cloning of nucleic acid involves mixing vectors comprising
PT recombination sites and/or nucleic acid, incubating mixture to produce
PT chimeric molecule, contacting hosts with mixture and selecting host.
XX
PS Claim 24; Col 46; 73pp; English.
XX
CC The present invention relates to a method for in vitro cloning of a
CC nucleic acid of interest. The method involves mixing in vitro two vectors
CC each comprising at least one recombination site and the nucleic acid of
CC interest; incubating the mixture in the presence of at least one
CC recombination protein to result in recombination of the recombination
CC sites, leading to production of a chimeric nucleic acid molecule
CC comprising the nucleic acid of interest; contacting hosts with the
CC mixture; and selecting for a host comprising the chimeric nucleic acid
CC molecule, and selecting against a host comprising the vectors comprising
CC the second vector, to clone the nucleic acid. The present sequence is a
CC recombination site, which may be used in the method of the present
CC invention
XX
SQ Sequence 25 BP; 4 A; 3 C; 4 G; 8 T; 0 U; 6 Other;
Query Match 86.4%; Score 21.6; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTYYKTRTACNAAAGTSG 25
DB 1 GTTCAGCTTYYKTRTACNAAAGTSG 25
RESULT 7
AAD14433
ID AAD14433 standard; DNA; 25 BP.
XX
AC AAD14433;
XX
DT 01-NOV-2001 (first entry)
DE Recombination site m-attP1 DNA.
XX
KW Recombination site; copy number; replicon; recombinatorial cloning;
KW m-attP1; ds.
XX
OS Unidentified.
XX
PN US6270969-B1.
XX
PD 07-AUG-2001.
XX
PF 20-JAN-1999; 99US-00233492.
XX
PR 07-JUN-1995; 95US-00486139.
PR 07-JUN-1996; 96US-00663002.
XX
PA (INVI-) INVITROGEN CORP.
XX
PI Hartley JL, Brasch MA;
XX WPI; 2001-488248/53.
XX
PT Methods for apposing nucleic acids comprising an expression signal and a
PT gene/partial gene, using recombinatorial cloning by incubating the
PT nucleic acids in the presence of a recombination protein under conditions
PT for recombination.
XX
PS Claim 14; Col 18; 76pp; English.
XX
CC The invention relates to a method for apposing an expression signal and a

CC gene or partial gene, using recombinatorial cloning. The method incubates
CC nucleic acids comprising the expression signal and the gene/partial gene
CC in the presence of a recombination protein under conditions sufficient to
CC cause recombination and therefore appose the expression signal and the
CC gene or partial gene. The methods are useful for apposing an expression
CC signal and a gene or partial gene using recombinatorial cloning. The
CC methods are also useful for changing vectors, constructing genes for
CC fusion proteins, changing copy number, changing replicons, cloning into
CC phages, and cloning e.g., PCR products (with an attB site at one end and
CC a loxP site at the other end), genomic DNAs, and cDNAs. The methods are
CC highly specific, rapid, and less labour intensive than prior art methods.
CC The present sequence is a recombination site useful for recombination
CC cloning
XX
SQ Sequence 25 BP; 4 A; 3 C; 4 G; 8 T; 0 U; 6 Other;
Query Match 86.4%; Score 21.6; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTYYKTRTACNAAAGTSG 25
DB 1 GTTCAGCTTYYKTRTACNAAAGTSG 25
RESULT 8
ABT16625
ID ABT16625 standard; DNA; 25 BP.
XX
AC ABT16625;
XX
DT 03-APR-2003 (first entry)
XX
DE Artificial plant chromosome related oligo SEQ ID No 37.
XX
KW Plant artificial chromosome; PAC; transgenic plant; vaccine;
KW blood factor; herbicide; stress; agronomical; nutrient quality;
KW bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
KW ds.
XX
OS Unidentified.
XX
PN WO200296923-A1.
XX
PD 05-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-US017451.
XX
PR 30-MAY-2001; 2001US-0294697P.
PR 04-JUN-2001; 2001US-0296329P.
XX
PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
PA (AGRI-) AGRISOMA INC.
XX
PI Perez C, Fabijanski SF, Perkins E;
XX WPI; 2003-140436/13.
XX
PT Producing artificial chromosome by introducing a nucleic acid into plant
PT cell, selecting artificial chromosome that has one or more repeat regions
PT with equivalent amounts of euchromatic and heterochromatic nucleic acids.
XX
PS Disclosure; Page 262; 269pp; English.
XX
CC The invention relates to a novel method for producing plant artificial
CC chromosomes. The invention also relates to methods for targeting
CC insertion of heterologous DNA into plant artificial chromosomes, methods
CC for delivery of plant chromosomes to selected cells and tissues. The
CC isolated plant artificial chromosome (PAC) is useful for producing a
CC transgenic plant, which involves introducing the PAC into a plant cell.
CC The PAC comprises a heterologous nucleic acid encoding a gene product
CC such as enzymes, antisense RNA, rDNA, structural proteins, marker
CC proteins, ligands, receptors, ribozymes, therapeutic proteins, and

CC biopharmaceutical proteins, vaccines, blood factors, antigens, hormones,
CC cytokines, growth factors, antibodies, or a product that provides for
CC resistance to diseases, insects, herbicides, or stress in a plant. The
CC heterologous nucleic acid optionally encodes a product that provides an
CC agronomically important trait in the plant, e.g. a product that alters
CC nutrient use and/or improves the nutrient quality of the plant. The
CC heterologous nucleic acid is contained within a bacterial artificial
CC chromosome (BAC) or a yeast artificial chromosome (YAC). This
CC polynucleotide sequence represents an oligo relating to the method for
CC producing plant artificial chromosomes of the invention
XX

SQ Sequence 25 BP; 4 A; 3 C; 4 G; 8 T; 0 U; 6 Other;

Query Match 86.4%; Score 21.6; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTKRTACNAAGTSG 25

Db 1 GTTCAGCTTTTKRTACNAAGTSG 25

RESULT 9

ACD28280
ID ACD28280 standard; DNA; 25 BP.

XX

AC ACD28280;

XX

DT 02-OCT-2003 (first entry)

XX

DE Nucleic acid core region m-attP1.

XX

KW Core region; ds; vector donor DNA; flanking recombination site; m-attP1.

XX

OS Synthetic.

XX

PN US2003064515-A1.

XX

PD 03-APR-2003.

XX

PF 30-JAN-2002; 2002US-00058291.

XX

PR 07-JUN-1995; 95US-00486139.

PR 07-JUN-1996; 96US-00663002.

PR 20-JAN-1999; 99US-00233493.

PR 02-NOV-1999; 99US-00432085.

XX

PA (HARTLEY) HARTLEY J L.

PA (BRASCH) BRASCH M A.

XX

FI Hartley JL, Brasch MA;

XX

DR WPI; 2003-540791/51.

XX

XX New Vector Donor DNA molecule for recombinational cloning using

PT engineered recombination sites, comprises first and second DNA segments
PT that do not recombine with each other and that contain a Selectable
PT marker.

XX

PS Claim 14; Page 25; 71pp; English.

XX

XX The invention relates to a vector donor DNA molecule comprising a first
CC DNA segment and a second DNA segment containing at least one selectable
CC marker. The first and second segments are separated either by, in a
CC circular vector donor, a first and a second recombination site, or in a
CC linear vector donor, at least a first recombination site, where each pair
CC of flanking recombination sites are engineered and do not recombine with
CC each other. The nucleic acid molecule, vectors and methods are useful for
CC moving or exchanging segments of DNA molecules using engineered
CC recombination sites and recombination proteins to provide chimeric DNA
CC molecules that have the desired characteristic(s) and/or DNA segment(s).
CC The present sequence represents the nucleic acid core region m-attP1

XX

SQ Sequence 25 BP; 4 A; 3 C; 4 G; 8 T; 0 U; 6 Other;

Query Match 86.4%; Score 21.6; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTKRTACNAAGTSG 25

Db 1 GTTCAGCTTTTKRTACNAAGTSG 25

RESULT 10

ACD28480

ID ACD28480 standard; DNA; 25 BP.

XX

AC ACD28480;

XX

DT 09-OCT-2003 (first entry)

XX

DE Nucleic acid core sequence m-attP1.

XX

KW Nucleic acid core; m-attP1; cointegrate DNA; flanking recombination site;
KW ds.

XX

OS Synthetic.

XX

PN US2003068799-A1.

XX

PD 10-APR-2003.

XX

PF 06-JUN-2002; 2002US-00162879.

XX

PR 07-JUN-1995; 95US-00486139.

PR 07-JUN-1996; 96US-00663002.

PR 20-JAN-1999; 99US-00233493.

PR 02-NOV-1999; 99US-00432085.

XX

PA (INVI-) INVITROGEN CORP.

XX

PI Hartley JL, Brasch MA;

XX

DR WPI; 2003-540884/51.

XX

XX Making CoIntegrate DNA molecule, by combining recombination sites
PT flanking the desired DNA segment in insert donor DNA, with the
PT recombination sites of vector donor DNA, using site specific
PT recombination protein.

XX

PS Claim 14; Page 25; 71pp; English.

XX

XX The invention relates to a method of making a coIntegrate DNA molecule.
CC The method is useful for making a coIntegrate DNA molecule. The method is
CC useful for a variety of DNA exchanges, such as subcloning of DNA, in
CC vitro or in vivo. The method enables efficient and specific recombination
CC of DNA segments using recombination proteins. The method is highly
CC specific, rapid and less labour intensive. The improved specificity,
CC yield and speed of the method facilitates DNA or RNA subcloning,
CC regulation and exchange useful for other related purposes. Since single
CC molecules of the recombinations product can be introduced into a
CC biological host, propagation of the desired product DNA in the absence of
CC other DNA molecules is more readily realised. Reaction conditions can be
CC freely adjusted in vitro to optimise enzyme activities. The present
CC sequence represents the nucleic acid core sequence m-attP1

XX

SQ Sequence 25 BP; 4 A; 3 C; 4 G; 8 T; 0 U; 6 Other;

Query Match 86.4%; Score 21.6; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTKRTACNAAGTSG 25

Db 1 GTTCAGCTTTTKRTACNAAGTSG 25

RESULT 11
ADA38166
ID ADA38166 standard; DNA; 25 BP.
XX
AC ADA38166;
XX
DT 20-NOV-2003 (first entry)
XX
DE m-attP1 DNA sequence indicating generic core region of an attP1 site.
XX
KW engineered recombination site; cloning; recombinase; subcloning; attB;
KW attP; attL; attR; selectable marker; cointegrate; m-attP1; ds.
XX
OS Synthetic.
XX
PN US2003054552-A1.
XX
PD 20-MAR-2003.
XX
PF 30-JAN-2002; 2002US-00058292.
XX
PR 07-JUN-1995; 95US-00486139.
PR 07-JUN-1996; 96US-00663002.
PR 20-JAN-1999; 99US-00233493.
PR 02-NOV-1999; 99US-00432085.
XX
PA (HART/) HARTLEY J L.
PA (BRAS/) BRASCH M A.
XX
PI Hartley JL, Brasch MA;
XX
DR WPI; 2003-585168/55.
XX
PS New Vector Donor DNA molecule, useful for recombinational cloning
PT purposes, comprises a first and a second DNA segment that contains a
PT selectable marker and is separated by a pair of flanking, engineered
PT recombination sites.
XX
PS Claim 14; Page 26; 72pp; English.
XX
CC This invention relates to novel DNA and vectors having engineered
CC recombination sites for use in a cloning method that enables efficient
CC and specific recombination of DNA segments using recombination proteins
CC including recombinases. As such, it provides a method for obtaining
CC chimeric nucleic acids with the desired characteristics, facilitating DNA
CC or RNA subcloning, regulation and/or exchange. The recombination site is
CC derived from attB, attP, attL or attR, where the att site is attL, att2 or
CC att3. Engineered mutations of the att sites (either one or multiple
CC mutations) can enhance specificity or efficiency of the recombination
CC reaction and the properties of the product DNA molecules. Accordingly,
CC the present invention describes a nucleic acid molecule comprising at
CC least one DNA segment having at least two engineered recombination sites
CC flanking a selectable marker and/or a desired DNA segment. Furthermore,
CC at least one of the engineered sites must enhance recombination in vitro
CC to form a cointegrate or product DNA molecule. This oligonucleotide
CC sequence is m-attP1, a generic DNA sequence indicating the core region of
CC an attP1 recombination site of the invention.
XX
SQ Sequence 25 BP; 4 A; 3 C; 4 G; 8 T; 0 U; 6 Other;
Query Match 86.4%; Score 21.6; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTTCAGCTTTTKRTACNAAGTSGB 25
Dy 1 GTTCAGCTTTTKRTACNAAGTSGB 25

RESULT 12
AAD60562

ID AAD60562 standard; DNA; 25 BP.
XX
AC AAD60562;
XX
DT 18-DEC-2003 (first entry)
XX
DE Core region DNA, m-attP1.
XX
KW Recombinational cloning; DNA exchange; core region; ds.
XX
OS Unidentified.
XX
PN US2003100110-A1.
XX
PD 29-MAY-2003.
XX
PF 02-NOV-1999; 99US-00432085.
PR 07-JUN-1995; 95US-00486139.
PR 07-JUN-1996; 96US-00663002.
PR 20-JAN-1999; 99US-00233493.
XX
PA (HART/) HARTLEY J L.
PA (BRAS/) BRASCH M A.
XX
PI Hartley JL, Brasch MA;
XX
DR WPI; 2003-730143/69.
XX
PS New Vector Donor DNA molecule for recombinational cloning using
PT engineered recombination sites, comprises first and second DNA segments
PT that do not recombine with each other and that contain a Selectable
PT marker.
XX
PS Claim 14; Page 25; 71pp; English.
XX
CC The invention relates to a vector donor DNA molecule which comprises
CC first and second DNA segments that do not recombine with each other and
CC that contain a selectable marker. The invention also relates to a method
CC for recombinational cloning using engineered recombination sites. The
CC invention is useful for moving or exchanging segments of DNA molecules
CC using engineered recombination sites and recombination proteins to
CC provide chimeric DNA molecules that have the desired characteristic(s)
CC and/or DNA segment(s). The present sequence is a core region DNA. This
CC sequence is used to illustrate the method of the invention
XX
SQ Sequence 25 BP; 4 A; 3 C; 4 G; 8 T; 0 U; 6 Other;
Query Match 86.4%; Score 21.6; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTTCAGCTTTTKRTACNAAGTSGB 25
Dy 1 GTTCAGCTTTTKRTACNAAGTSGB 25

RESULT 13

ABZ58738

ID ABZ58738 standard; DNA; 25 BP.
XX
AC ABZ58738;
XX
DT 01-MAY-2003 (first entry)
XX
DE Att site nucleotide sequence attR2.
XX
KW Nucleic acid insertion; recombination; nucleic acid selection;
KW nucleic acid isolation; att; ds.
XX
OS Synthetic.
XX
PN WO200295055-A2.

```

XX PD 28-NOV-2002.
XX PF 21-MAY-2002; 2002WO-US015947.
XX PR 21-MAY-2001; 2001US-0291973P.
XX PA (INVI-) INVITROGEN CORP.
XX PI Braach MA, Cheo D, Li X, Eposito D, Byrd DRN;
XX DR WPI; 2003-129436/12.
XX XX Inserting a population of nucleic acids into a second target molecule for
PT selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid.
XX PS Disclosure; Fig 13A; 273pp; English.
XX CC The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. Sequences ABZ58727-762
CC represent att recombination site sequences used in the method of the
CC invention
XX SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 U; 0 Other;

Query Match 86.4%; Score 21.6; DB 10; Length 25;
Best Local Similarity 76.0%; Pred. No. 2.2;
Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GTTCAGCTTTVKTACNAAGTSGB 25
Db 1 GTTCAGCTTTCTGTACAAAGTGGT 25

RESULT 14
AC ACC59582 standard; DNA; 25 BP.
XX AC ACC59582;
XX DT 08-SEP-2003 (first entry)
XX DE Nucleic acid preparation method att site SEQ ID NO: 30.
XX KW Nucleic acid preparation; cloning; mutagenesis; adaptor; cleavage site;
XX genetic engineering; PCR; primer; adaptor; ss.
XX OS Bacteriophage lambda.
XX PN WO200304207-A2.
XX PD 30-MAY-2003.
XX PF 22-NOV-2002; 2002WO-IB005316.
XX PR 22-NOV-2001; 2001JP-00357821.
XX PA (INVI-) INVITROGEN JAPAN KK.
XX PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX PI Nomura N, Goshima N, Kisu Y, Sono S;
XX WPI; 2003-457615/43.

XX XX Preparing nucleic acids for genetic analyses comprises contacting a
PT template nucleic acid molecule with a primer and a polypeptide having DNA
PT polymerase activity to form a mixture, and incubating the mixture to
PT extend the primer.
XX PS Disclosure; Page 36; 81pp; English.
XX CC The present invention relates to a method of preparing nucleic acid
CC molecules, which comprises contacting a template nucleic acid molecule
CC with a first, second and third primer and a polypeptide with DNA
CC polymerase activity to form a mixture and incubating the mixture to
CC extend the primers. The method is useful in genetic engineering,
CC particularly in the amplification, rapid cloning and mutagenesis of
CC nucleic acid molecules for genetic analyses. The present sequence is an
CC oligonucleotide shown in the exemplification of the invention
XX SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 U; 0 Other;

Query Match 86.4%; Score 21.6; DB 10; Length 25;
Best Local Similarity 76.0%; Pred. No. 2.2;
Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GTTCAGCTTTVKTACNAAGTSGB 25
Db 1 GTTCAGCTTTCTGTACAAAGTGGT 25

RESULT 15
AC ACC44654 standard; DNA; 25 BP.
XX AC ACC44654;
XX DT 29-MAY-2003 (first entry)
XX DE Recombination site related oligonucleotide SEQ ID NO:45.
XX KW Chromosome-based platform; artificial chromosome; eukaryotic chromosome;
XX att site; integrase; recombinase; ACes; gene therapy; transgenic animal;
XX platform artificial chromosome expression system; PCR primer; ss.
XX OS Synthetic.
XX PN WO200297059-A2.
XX PD 05-DEC-2002.
XX PF 30-MAY-2002; 2002WO-US017452.
XX PR 30-MAY-2001; 2001US-0294758P.
XX PR 21-MAR-2002; 2002US-0366891P.
XX PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
XX PI Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;
XX PI Stewart S, Shellard J;
XX WPI; 2003-140461/13.
XX PT Novel eukaryotic chromosome comprising one or many att sites which
PT permits site-directed integration in the presence of lambda-integrase,
PT useful for site-specific recombination-directed integration of DNA of
PT interest.
XX PS Claim 43; Page 143; 272pp; English.
XX CC The present invention describes a eukaryotic chromosome (I) comprising
CC one or several att sites, where an att site is heterologous to the
CC chromosome, and permits site-directed integration in the presence of
CC lambda-integrase. Also described: (1) a platform artificial chromosome
CC expression system (ACes) (II) comprising several sites that participate
CC in recombinase catalysed recombination; and (2) a method (M1) for

```

CC introducing a heterologous nucleic acid into a platform artificial
CC chromosome. (i) can be used in gene therapy. (M1) is useful for
CC introducing a heterologous nucleic acid molecule into a platform
CC artificial chromosome, preferably an ACes. (II) is useful for producing a
CC transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or
CC mammal) by introducing (ii) by cell fusion, lipid-mediated transfection
CC by a carrier system, microinjection, microcell fusion, electroporation,
CC microprojectile bombardment or direct DNA transfer into an embryonic
CC cell, preferably a stem cell or an embryo. (II) comprises a heterologous
CC nucleic acid that encodes a therapeutic product which is useful for
CC making a library of ACes comprising random portions of a genome. ACC44612
CC to ACC44732 and ABP9650 to ABP9657 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 25 BP; 4 A; 3 C; 4 G; 8 T; 0 U; 6 Other;

Query Match 86.4%; Score 21.6; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTTCAGCTTYYKTRTACNAAGTSGB 25
|||||
Db 1 GTTCAGCTTYYKTRTACNAAGTSGB 25

Search completed: November 16, 2004, 04:02:48
Job time : 168.8 secs

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:19 ; Search time 35.9 Seconds
(without alignments)
494.978 Million cell updates/sec

Title: US-10-820-133-5

Perfect score: 25

Sequence: 1 gttcagcttcttactacnaagtsb 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21.6	86.4	25	3	US-09-233-493-5
2	21.6	86.4	25	3	US-09-005-476-5
3	21.6	86.4	25	3	US-09-233-492-5
4	21.6	86.4	25	3	US-09-296-280-5
5	21.6	86.4	25	3	US-09-296-280-11
6	21.6	86.4	25	4	US-09-498-074-5
7	21.6	86.4	25	4	US-09-498-074-5
8	21.6	86.4	25	5	PCT-US96-10082A-5
9	21.2	84.8	25	3	US-09-296-280-42
10	20.4	81.6	25	3	US-09-233-493-11
11	20.4	81.6	25	3	US-09-233-493-15
12	20.4	81.6	25	3	US-09-233-493-16
13	20.4	81.6	25	3	US-09-005-476-11
14	20.4	81.6	25	3	US-09-005-476-15
15	20.4	81.6	25	3	US-09-005-476-16
16	20.4	81.6	25	3	US-09-233-492-11
17	20.4	81.6	25	3	US-09-233-492-15
18	20.4	81.6	25	3	US-09-233-492-16
19	20.4	81.6	25	3	US-09-296-280-15
20	20.4	81.6	25	3	US-09-296-280-16
21	20.4	81.6	25	3	US-09-296-280-43
22	20.4	81.6	25	4	US-09-498-074-11
23	20.4	81.6	25	4	US-09-498-074-15
24	20.4	81.6	25	4	US-09-498-074-16
25	20.4	81.6	25	4	US-09-498-074-11
26	20.4	81.6	25	4	US-09-498-074-15
27	20.4	81.6	25	4	US-09-498-074-16

28	20.4	81.6	25	5	PCT-US96-10082A-11	Sequence 11, Appl
29	20.4	81.6	25	5	PCT-US96-10082A-15	Sequence 15, Appl
30	20.4	81.6	25	5	PCT-US96-10082A-16	Sequence 16, Appl
31	20.4	81.6	201	1	US-08-021-667A-18	Sequence 18, Appl
32	20.4	81.6	201	1	US-08-410-544-18	Sequence 18, Appl
33	20.4	81.6	201	1	US-08-728-785A-18	Sequence 18, Appl
34	20.4	81.6	1763	4	US-09-244-805-57	Sequence 57, Appl
35	20.4	81.6	4909	3	US-08-556-978B-78	Sequence 78, Appl
36	20.4	81.6	6043	4	US-09-630-929-4	Sequence 4, Appl
37	20.4	81.6	7652	1	US-07-590-988A-1	Sequence 1, Appl
38	20	80.0	25	3	US-09-233-493-3	Sequence 3, Appl
39	20	80.0	25	3	US-09-005-476-3	Sequence 3, Appl
40	20	80.0	25	3	US-09-233-492-3	Sequence 3, Appl
41	20	80.0	25	3	US-09-296-280-3	Sequence 3, Appl
42	20	80.0	25	4	US-09-498-074-3	Sequence 3, Appl
43	20	80.0	25	4	US-09-498-074-3	Sequence 3, Appl
44	20	80.0	25	5	PCT-US96-10082A-3	Sequence 3, Appl
45	19.6	78.4	25	3	US-09-233-493-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-233-493-5
; Sequence 5, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-493-5

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Query Match      86.4%; Score 21.6; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTYYKTRTACNAAGTSGB 25
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Db 1 GTTCAGCTTYYKTRTACNAAGTSGB 25

RESULT 2
US-09-005-476-5
; Sequence 5, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2600
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-5

Query Match      86.4%; Score 21.6; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTYYKTRTACNAAGTSGB 25
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Db 1 GTTCAGCTTYYKTRTACNAAGTSGB 25

RESULT 3
US-09-233-492-5
; Sequence 5, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
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; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-492-5

Query Match      86.4%; Score 21.6; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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    |||||
Db 1 GTTCAGCTTYYKTRTACNAAGTSGB 25

RESULT 4
US-09-296-280-5
; Sequence 5, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942,2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-5
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Query Match 86.4%; Score 21.6; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0;

Oy 1 GTTCAGCTTTTKRTACNAAGTSG 25
Db 1 GTTCAGCTTTTKRTACNAAGTSG 25

RESULT 5

US-09-296-280-11
; Sequence 11, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296.280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 11
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-11

Query Match 86.4%; Score 21.6; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.3;
Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GTTCAGCTTTTKRTACNAAGTSG 25
Db 1 GTTCAGCTTTCTGTACAAAGTGT 25

RESULT 6

US-09-498-074-5
; Sequence 5, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:

TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-498-074-5

Query Match 86.4%; Score 21.6; DB 4; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.3; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0;

Oy 1 GTTCAGCTTTTKRTACNAAGTSG 25
Db 1 GTTCAGCTTTTKRTACNAAGTSG 25

RESULT 7

US-09-498-074-5
; Sequence 5, Application US/09498074
; Patent No. 6720140
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: 04-Feb-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid

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; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-498-074-5

Query Match      86.4%; Score 21.6; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GTTCAGCTTTTXYKTRTACNAAGTSGB 25

RESULT 8
PCT-US96-10082A-5
; Sequence 5, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
; APPLICANT: Gaithersburg, MD 20884-9980
; APPLICANT: United States of America
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10082A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
PCT-US96-10082A-5

Query Match      86.4%; Score 21.6; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTXYKTRTACNAAGTSGB 25
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DB 1 GTTCAGCTTTTXYKTRTACNAAGTSGB 25

RESULT 9
US-09-296-280-42
; Sequence 42, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.

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; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-493-11

Query Match      81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.1;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTCTGTACAAAGTGG 25
Db 1 GTTCAGCTTTTCTGTACAAAGTGG 25

RESULT 11
US-09-233-493-15
; Sequence 15, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233.493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005.476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663.002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486.139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-493-15

Query Match      81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.1;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTCTGTACAAAGTGG 25
Db 1 GTTCAGCTTTTCTGTACAAAGTGG 25

RESULT 12
US-09-233-493-16
; Sequence 16, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233.493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005.476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663.002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
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; APPLICATION NUMBER: 08/486.139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-493-16

Query Match      81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.1;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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Db 1 GTTCAGCTTTTCTGTACAAAGTGG 25

RESULT 13
US-09-005-476-11
; Sequence 11, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
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; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-11

Query Match      81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.1;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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Db      1 GTTCAGCTTCTGTGACAAAGTTGG 25

RESULT 14
US-09-005-476-15
; Sequence 15, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
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; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-15

Query Match      81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.1;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GTTCAGCTTYYKTRTACNAAGTSG 25
Db      1 GTTCAGCTTCTGTGACAAAGTTGG 25

RESULT 15
US-09-005-476-16
; Sequence 16, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-16

Query Match      81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.1;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GTTCAGCTTYYKTRTACNAAGTSG 25
Db      1 GTTCAGCTTCTGTGACAAAGTTGG 25

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Job time : 36.9 secs
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:34:49 ; Search time 314 Seconds
(without alignments)
430.015 Million cell updates/sec

Title: US-10-820-133-5

Perfect score: 25

Sequence: 1 gttcagcttktttacnaagtsb 25

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Gapop 10.0 , Gapext 1.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications NA:*

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21: /cgn2_6/ptodata/1/pubna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	21.6	86.4	25	9	US-09-855-797A-5
3	21.6	86.4	25	9	US-09-855-797A-11
4	21.6	86.4	25	9	US-09-907-900-5
5	21.6	86.4	25	9	US-09-907-900-11
6	21.6	86.4	25	9	US-09-907-719-5
7	21.6	86.4	25	9	US-09-907-719-11
8	21.6	86.4	25	10	US-09-432-085-5
9	21.6	86.4	25	10	US-09-985-448-5
10	21.6	86.4	25	10	US-09-985-448-11
11	21.6	86.4	25	14	US-10-058-292-5
12	21.6	86.4	25	14	US-10-058-291-5

13	21.6	86.4	25	14	US-10-162-879-5	Sequence 5, Appli
14	21.6	86.4	25	15	US-10-161-403-45	Sequence 45, Appli
15	21.6	86.4	25	15	US-10-151-690-36	Sequence 36, Appli
16	21.6	86.4	25	15	US-10-300-892-5	Sequence 5, Appli
17	21.6	86.4	25	15	US-10-300-892-11	Sequence 11, Appli
18	21.6	86.4	25	16	US-10-301-849A-30	Sequence 30, Appli
19	21.6	86.4	25	16	US-10-680-316-5	Sequence 5, Appli
20	21.6	86.4	25	16	US-10-680-316-11	Sequence 11, Appli
21	21.6	86.4	25	17	US-10-815-730-5	Sequence 5, Appli
22	21.6	86.4	25	17	US-10-815-730-11	Sequence 11, Appli
23	21.6	86.4	25	17	US-10-820-133-5	Sequence 5, Appli
24	21.6	86.4	25	17	US-10-820-133-11	Sequence 11, Appli
25	21.6	86.4	25	18	US-10-161-408-37	Sequence 37, Appli
26	21.6	86.4	25	18	US-10-622-088-18	Sequence 18, Appli
27	21.6	86.4	25	18	US-10-796-868A-5	Sequence 5, Appli
28	21.6	86.4	158	15	US-10-403-232-183	Sequence 183, App
29	21.6	86.4	1846	15	US-10-023-208-63	Sequence 63, Appli
30	21.6	86.4	5038	18	US-10-622-088-89	Sequence 89, Appli
31	21.6	86.4	5148	11	US-09-860-763-10	Sequence 10, Appli
32	21.6	86.4	5375	17	US-10-612-410-5	Sequence 5, Appli
33	21.6	86.4	5558	15	US-10-241-596-137	Sequence 137, App
34	21.6	86.4	5693	18	US-10-622-088-90	Sequence 90, Appli
35	21.6	86.4	5763	18	US-10-622-088-94	Sequence 94, Appli
36	21.6	86.4	6464	15	US-10-151-690-20	Sequence 20, Appli
37	21.6	86.4	6959	17	US-10-612-410-3	Sequence 3, Appli
38	21.6	86.4	7278	16	US-10-097-034A-37	Sequence 37, Appli
39	21.6	86.4	7341	18	US-10-622-088-112	Sequence 112, App
40	21.6	86.4	7618	17	US-10-612-410-1	Sequence 1, Appli
41	21.6	86.4	7995	18	US-10-622-088-113	Sequence 113, App
42	21.6	86.4	8599	18	US-10-622-088-115	Sequence 115, App
43	21.6	86.4	8634	18	US-10-622-088-107	Sequence 107, App
44	21.6	86.4	8688	18	US-10-622-088-105	Sequence 105, App
45	21.6	86.4	9249	15	US-10-389-120-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-732-914-12

; Sequence 12, Application US/09732914

; Patent No. US20020007051A1

; GENERAL INFORMATION:

; APPLICANT: Cheo, David

; APPLICANT: Brasch, Michael A.

; APPLICANT: Temple, Gary F.

; APPLICANT: Hartley, James L.

; APPLICANT: Byrd, Devon R.N.

; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in

; FILE REFERENCE: 0942.5010002

; CURRENT APPLICATION NUMBER: US/09/732.914

; CURRENT FILING DATE: 2000-12-11

; PRIOR APPLICATION NUMBER: US 60/169,983

; PRIOR FILING DATE: 1999-12-10

; PRIOR APPLICATION NUMBER: US 60/188,020

; PRIOR FILING DATE: 2000-03-09

; NUMBER OF SEQ ID NOS: 140

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 12

; LENGTH: 25

; TYPE: DNA

; ORGANISM: attR2

US-09-732-914-12

Query Match	86.4%	Score 21.6;	DB 9;	Length 25;
Best Local Similarity	76.0%	Pred. No. 1.4;	Indels 0;	Gaps 0;
Matches	19;	Conservative	5;	Mismatches 1;
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Db	1	GTTCAGCTTTT	CTCTACAAAGTGT	25

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RESULT 2
US-09-855-797A-5
; Sequence 5, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.285008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-5

Query Match      86.4%; Score 21.6; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTXYKTRTACNAAAGTSG 25
Db 1 GTTCAGCTTTTXYKTRTACNAAAGTSG 25

RESULT 3
US-09-855-797A-11
; Sequence 11, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.285008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-11

Query Match      86.4%; Score 21.6; DB 9; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.4;
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Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTXYKTRTACNAAAGTSG 25
Db 1 GTTCAGCTTTTCTGTACAAAGTG 25

RESULT 4
US-09-907-900-5
; Sequence 5, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.285004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-5

Query Match      86.4%; Score 21.6; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTXYKTRTACNAAAGTSG 25
Db 1 GTTCAGCTTTTXYKTRTACNAAAGTSG 25

RESULT 5
US-09-907-900-11
; Sequence 11, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.285004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-11
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Query Match 86.4%; Score 21.6; DB 9; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.4;
Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

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DB 1 GTTCAGCTTCTTGTACAAAGTGGT 25

RESULT 6

US-09-907-719-5
; Sequence 5, Application US/09907719
; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Braesch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-719-5

Query Match 86.4%; Score 21.6; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GTTCAGCTTYYKTRTACNAAGTSG 25

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; Sequence 11, Application US/09907719
; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Braesch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 11
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products

US-09-907-719-11

Query Match 86.4%; Score 21.6; DB 9; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.4;
Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTYYKTRTACNAAGTSG 25
|||||:|||||:|||||:|||||:
DB 1 GTTCAGCTTCTTGTACAAAGTGGT 25

RESULT 8

US-09-432-085-5
; Sequence 5, Application US/09432085
; Publication No. US20030100110A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Braesch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-432-085-5

Query Match 86.4%; Score 21.6; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTYYKTRTACNAAGTSG 25
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DB 1 GTTCAGCTTYYKTRTACNAAGTSG 25

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RESULT 9
US-09-985-448-5
; Sequence 5, Application US/09985448
; Publication No. US20030157716A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/985,448
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 18
; OTHER INFORMATION: "n" may be any nucleotide
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-985-448-5

Query Match      86.4%; Score 21.6; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTXXRTACNAAGTSG 25
DB 1 GTTCAGCTTTTXXRTACNAAGTSG 25

RESULT 10
US-09-985-448-11
; Sequence 11, Application US/09985448
; Publication No. US20030157716A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/985,448
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-985-448-11

Query Match      86.4%; Score 21.6; DB 10; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.4; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTXXRTACNAAGTSG 25
DB 1 GTTCAGCTTTTXXRTACNAAGTSG 25
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Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTXXRTACNAAGTSG 25
DB 1 GTTCAGCTTTTCTGTACAAAGTGGT 25

RESULT 11
US-10-058-292-5
; Sequence 5, Application US/10058292
; Publication No. US20030054552A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/058,292
; FILING DATE: 30-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/432,085
; FILING DATE: 1999-11-02
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-058-292-5

Query Match      86.4%; Score 21.6; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GTTCAGCTTTTXXRTACNAAGTSG 25
DB 1 GTTCAGCTTTTXXRTACNAAGTSG 25

RESULT 12
US-10-058-291-5
; Sequence 5, Application US/10058291
; Publication No. US20030064515A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
```

;; TITLE OF INVENTION: Recombinational Cloning Using Engineered
;; Recombination Sites
;; NUMBER OF SEQUENCES: 35
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
;; STREET: 1100 New York Ave., N. W. Suite 600
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005-3934
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/058,291
;; FILING DATE: 30-Jan-2002
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/432,085
;; FILING DATE: 1999-11-02
;; APPLICATION NUMBER: 09/233,493
;; FILING DATE: 20-JAN-1999
;; APPLICATION NUMBER: 09/005,476
;; FILING DATE: 20-JAN-1999
;; APPLICATION NUMBER: 08/663,002
;; FILING DATE: 12-JAN-1998
;; APPLICATION NUMBER: 08/663,002
;; FILING DATE: 07-JUN-1996
;; APPLICATION NUMBER: 08/486,139
;; FILING DATE: 07-JUN-1995
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-058-291-5
Query Match 86.4%; Score 21.6; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTTCAGCTTYYKTRTACNAAGTSG 25
Db 1 GTTCAGCTTYYKTRTACNAAGTSG 25
RESULT 13
US-10-162-879-5
; Sequence 5, Application US/10162879
; Publication No. US20030068799A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Bransch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/162,879
;; FILING DATE: 06-Jun-2002
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/432,085
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: 09/233,493
;; FILING DATE: 20-JAN-1999
;; APPLICATION NUMBER: 09/005,476
;; FILING DATE: 12-JAN-1998
;; APPLICATION NUMBER: 08/663,002
;; FILING DATE: 07-JUN-1996
;; APPLICATION NUMBER: 08/486,139
;; FILING DATE: 07-JUN-1995
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 25 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; MOLECULE TYPE: cDNA
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-162-879-5
Query Match 86.4%; Score 21.6; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTTCAGCTTYYKTRTACNAAGTSG 25
Db 1 GTTCAGCTTYYKTRTACNAAGTSG 25
RESULT 14
US-10-161-403-45
; Sequence 45, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: m-attP1
; FEATURE:
; NAME/KEY: misc_difference
; LOCATION: 18
; OTHER INFORMATION: n is a or g or c or t/u
US-10-161-403-45

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Query Match      86.4%; Score 21.6; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTKYKTRTACNAAGTSG 25
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Db 1 GTTCAGCTTTKYKTRTACNAAGTSG 25

RESULT 15
US-10-151-690-36
; Sequence 36, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOL
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 25
; TYPE: DNA
; ORGANISM: attr2
US-10-151-690-36

Query Match      86.4%; Score 21.6; DB 15; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.4;
Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTKYKTRTACNAAGTSG 25
   |||||
Db 1 GTTCAGCTTTCTGTACAAAGTGGT 25

Search completed: November 16, 2004, 11:14:59
Job time : 314.1 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:04 ; Search time 1532 Seconds
(without alignments)
594.643 Million cell updates/sec

Title: US-10-820-133-5

Perfect score: 25

Sequence: 1 gttcagcttcttactacnaagtsb 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gse1:*

9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	21.6	86.4	753	8 AQ990861	AQ990861 Rfc01698
C 3	21.6	86.4	808	8 AQ990388	AQ990388 Rfc01153
C 4	20.6	82.4	719	8 AQ991352	AQ991352 Rfc02270
C 5	20.4	81.6	206	5 BQ156416	BQ156416 NF092F021
C 6	20.4	81.6	299	5 BQ115594	BQ115594 BY115594
C 7	20.4	81.6	306	5 BQ157615	BQ157615 BP757615
C 8	20.4	81.6	374	5 BP754432	BP754432 BP754432
C 9	20.4	81.6	401	5 BP754410	BP754410 BP754410
C 10	20.4	81.6	409	5 BP754552	BP754552 BP754552
C 11	20.4	81.6	422	5 BP754464	BP754464 BP754464
C 12	20.4	81.6	423	5 BP754551	BP754551 BP754551
C 13	20.4	81.6	430	5 BP754589	BP754589 BP754589
C 14	20.4	81.6	432	5 BP754563	BP754563 BP754563
C 15	20.4	81.6	443	5 BP754508	BP754508 BP754508
C 16	20.4	81.6	443	5 BP754571	BP754571 BP754571
C 17	20.4	81.6	449	5 BP754440	BP754440 BP754440
C 18	20.4	81.6	472	5 BQ157398	BQ157398 NF104D071
C 19	20.4	81.6	473	5 BQ156404	BQ156404 NF092E031
C 20	20.4	81.6	482	5 BP754592	BP754592 BP754592
C 21	20.4	81.6	483	5 BP757892	BP757892 BP757892
C 22	20.4	81.6	486	5 BP754503	BP754503 BP754503
C 23	20.4	81.6	489	5 BP754581	BP754581 BP754581
C 24	20.4	81.6	546	5 BP754439	BP754439 BP754439

C 25	20.4	81.6	567	5 BP754491	BP754491 BP754491
C 26	20.4	81.6	597	4 B1422679	B1422679 EST533345
C 27	20.4	81.6	645	5 BP754484	BP754484 BP754484
C 28	20.4	81.6	671	5 BP754388	BP754388 BP754388
C 29	20.4	81.6	672	5 BP754535	BP754535 BP754535
C 30	20.4	81.6	674	5 BP754519	BP754519 BP754519
C 31	20.4	81.6	689	5 BP754572	BP754572 BP754572
C 32	20.4	81.6	695	8 AQ991039	AQ991039 Rfc01894
C 33	20.4	81.6	712	8 AQ990809	AQ990809 Rfc01638
C 34	20.4	81.6	731	5 BP758121	BP758121 BP758121
C 35	20.4	81.6	743	8 AQ990346	AQ990346 Rfc01106
C 36	20.4	81.6	764	8 AQ990110	AQ990110 Rfc00827
C 37	20.4	81.6	769	8 AQ990470	AQ990470 Rfc01245
C 38	20	80.0	321	2 BF086649	BF086649 CMO-GN007
C 39	20	80.0	595	2 AW993039	AW993039 KC2-BN003
C 40	20	80.0	635	7 CN484020	CN484020 hw41b03.Y
C 41	20	80.0	675	8 AQ991241	AQ991241 Rfc02132
C 42	20	80.0	706	4 B1836912	B1836912 603084230
C 43	20	80.0	714	5 BX359053	BX359053 BX359053
C 44	20	80.0	752	4 BG620766	BG620766 602617479
C 45	20	80.0	797	4 BG427603	BG427603 602497040

ALIGNMENTS

RESULT 1
AQ990864/c
LOCUS
DEFINITION
672 bp DNA linear GSS 14-AUG-2000
Phototaxhabdus luminescens strain W14 M13 library
Phototaxhabdus luminescens genomic clone PLG01701, genomic survey
sequence.
ACCESSION
AQ990864
VERSION
AQ990864.1
KEYWORDS
GSS.
SOURCE
Phototaxhabdus luminescens
ORGANISM
Phototaxhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Phototaxhabdus.
REFERENCE
1 (bases 1 to 672)
ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
A genomic sample sequence of the entomopathogenic bacterium
Phototaxhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
20378633
10919786
Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsarfbath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to B.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.
Location/Qualifiers
1. .672
/organism="Phototaxhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clones="PLG01701"
/dev_stage="primary phase variant"
/clone_lib="Phototaxhabdus luminescens strain W14 M13
library"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

FEATURES

source
1. .672
/organism="Phototaxhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clones="PLG01701"
/dev_stage="primary phase variant"
/clone_lib="Phototaxhabdus luminescens strain W14 M13
library"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

ORIGIN

Query Match 86.4%; Score 21.6; DB 8; Length 672;
 Best Local Similarity 76.0%; Pred. No. 19;
 Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTYYKTRTACNAAGTSGB 25
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 Db 637 GTTCAGCTTTTATATAAGTGGC 613

RESULT 2
 AQ990861/c
 LOCUS
 DEFINITION
 Rfc01698 Photorhabdus luminescens strain W14 M13 library
 Photorhabdus luminescens genomic clone PLG01698, genomic survey
 sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Photorhabdus luminescens
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Photorhabdus.

REFERENCE
 AUTHORS
 1 (bases 1 to 753)
 fFrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
 Daborn,P.J., Bowen,D. and Blattner,F.R.
 A genomic sample sequence of the entomopathogenic bacterium
 Photorhabdus luminescens W14: potential implications for virulence
 Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

JOURNAL
 MEDLINE
 PUBMED
 COMMENT
 20378633
 10919786
 Contact: fFrench-Constant RH
 Department of Biology and Biochemistry
 University of Bath
 South Building, Bath BA2 7AY, UK
 Tel: (44) 1225 826621
 Fax: (44) 1225 826779
 Email: bsarfcbath.ac.uk
 This is one of 2,122 random reads from the M13 library. For
 annotation of identified clones (BLASTX, BLASTN and mapping to E.
 coli K12 genome) please see fFrench-Constant et al. 2000, Nucleic
 Acids Res.

Seq primer: M13 Forward
 Class: shotgun.

FEATURES
 source

Location/Qualifiers
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 /organism="Photorhabdus luminescens"
 /mol_type="genomic DNA"
 /strain="W14"
 /db_xref="taxon:29488"
 /clone="PLG01698"
 /dev_stage="primary phase variant"
 /clone_lib="Photorhabdus luminescens strain W14 M13
 library"
 /note="Genomic DNA from strain W14 was size selected (1-2
 kb) and then cloned into M13 Janus."

ORIGIN
 Query Match 86.4%; Score 21.6; DB 8; Length 753;
 Best Local Similarity 76.0%; Pred. No. 19;
 Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTYYKTRTACNAAGTSGB 25
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 Db 638 GTTCAGCTTTTATATAAGTGGC 614

RESULT 3
 AQ990388/c
 LOCUS
 DEFINITION
 Rfc01153 Photorhabdus luminescens strain W14 M13 library
 Photorhabdus luminescens genomic clone PLG01153, genomic survey
 sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Photorhabdus luminescens
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Photorhabdus.

REFERENCE
 AUTHORS
 1 (bases 1 to 808)
 fFrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
 Daborn,P.J., Bowen,D. and Blattner,F.R.
 A genomic sample sequence of the entomopathogenic bacterium
 Photorhabdus luminescens W14: potential implications for virulence
 Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

JOURNAL
 MEDLINE
 PUBMED
 COMMENT
 20378633
 10919786
 Contact: fFrench-Constant RH
 Department of Biology and Biochemistry
 University of Bath
 South Building, Bath BA2 7AY, UK
 Tel: (44) 1225 826621
 Fax: (44) 1225 826779
 Email: bsarfcbath.ac.uk
 This is one of 2,122 random reads from the M13 library. For
 annotation of identified clones (BLASTX, BLASTN and mapping to E.
 coli K12 genome) please see fFrench-Constant et al. 2000, Nucleic
 Acids Res.

Seq primer: M13 Forward
 Class: shotgun.

FEATURES
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 Location/Qualifiers
 1..808
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 /db_xref="taxon:29488"
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 library"
 /note="Genomic DNA from strain W14 was size selected (1-2
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ORIGIN
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 Best Local Similarity 76.0%; Pred. No. 19;
 Matches 19; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTYYKTRTACNAAGTSGB 25
 |||||:||||:||||:||||:||||:||||:
 Db 628 GTTCAGCTTTTATATAAGTGGC 604

RESULT 4
 AQ991352/c
 LOCUS
 DEFINITION
 Rfc02270 Photorhabdus luminescens strain W14 M13 library
 Photorhabdus luminescens genomic clone PLG02270, genomic survey
 sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Photorhabdus luminescens
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Photorhabdus.

REFERENCE
 AUTHORS
 1 (bases 1 to 719)
 fFrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
 Daborn,P.J., Bowen,D. and Blattner,F.R.
 A genomic sample sequence of the entomopathogenic bacterium
 Photorhabdus luminescens W14: potential implications for virulence
 Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

JOURNAL
 MEDLINE
 PUBMED
 COMMENT
 20378633
 10919786
 Contact: fFrench-Constant RH

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Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsearfbath.ac.uk

This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see firench-Constant et al. 2000, Nucleic
Acids Res.

Seq primer: M13 Forward

Class: shotgun.

Location/Qualifiers

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/organism="Photorhabdus luminescens"
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/clone="PIG02270"
/dev_stage="primary phase variant"
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library"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

FEATURES
source

ORIGIN

Query Match 82.4%; Score 20.6; DB 8; Length 719;
Best Local Similarity 72.0%; Pred. No. 57;
Matches 18; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GTTCAGCTTTTKTRTACNAAGTSGB 25
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Db 638 GTTCAGCTTTTATANTAGTGC 614

RESULT 5

BQ156416/c
LOCUS BQ156416 206 bp mRNA linear EST 24-APR-2002
DEFINITION NF092F02IR1F1027 Irradiated Medicago truncatula cDNA clone
NF092F02IR 5', mRNA sequence.
ACCESSION BQ156416
VERSION BQ156416.1 GI:20293475
KEYWORDS Medicago truncatula (barrel medic)
SOURCE Medicago truncatula
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 206)
Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula irradiated library
Unpublished (2001)
CONTACT: May GD
PLANT Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 224 6650
Fax: 580 224 6692
Email: gdmay@noble.org
Insert Length: 206 Std Error: 0.00
Plate: 092 row: F column: 02
Seq primer: TCACACAGGAACACTATGAC.

Location/Qualifiers
1..206
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/clone="NF092F02IR"
/tissue_type="seedlings"
/dev_stage="seedling"

FEATURES
source

/clone_lib="Irradiated"
/note="Vector: Lambda Zap; Seedlings were exposed either
to 100 Gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation.
Gamma-irradiated samples were harvested at 6, 12, 24 and
48 hours after treatment. UV-irradiated samples were
harvested 24 hours post-treatment. cDNA was prepared from
polyA+ enriched, pooled samples of equivalent amounts of
total RNA from each sample. The cDNA was directionally
ligated into the Uni-Zap XR vector (Stratagene) and
packaged using the Gigapack III Gold packaging extracts.
Phagemids containing cDNA inserts were in vivo excised
from the recombinant Uni-Zap XR vector using ExAssist
helper phage and the E. coli strain XL1-Blue MRF'
(Stratagene). Excised plasmids were plated using SOLR
cells."

ORIGIN

Query Match 81.6%; Score 20.4; DB 5; Length 206;
Best Local Similarity 76.0%; Pred. No. 60;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GTTCAGCTTTTKTRTACNAAGTSGB 25
|||||:|||||:|||||:|||||:
Db 167 GTTCAGCTTTTATACTAAGTTCG 143

RESULT 6

BQ115594
LOCUS BQ115594 299 bp mRNA linear EST 08-DEC-2002
DEFINITION BQ115594 RIKEN full-length enriched, 18 days embryo whole body Mus
musculus cDNA clone L430040C03 5', mRNA sequence.
ACCESSION BQ115594
VERSION BQ115594.1 GI:26226695
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 299)
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
Nikaido,I., Osato,N., Saito,R., Yamanaoka,I.,
Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
Fletcher,C.F., Forrest,A., Frazer,K.S., Gassterland,T.,
Gariboldi,M., Giasi,C., Godzik,A., Gough,J., Grimmond,S.,
Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konegaya,A.,
Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
Verardo,R., Wagner,L., Wahlstedt,C., Wang,Y., Watanabe,Y.,
Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
JOURNAL MEDLINE
NATURE 22354683
PUBMED 12466851

CONTACT: Yoshihide Hayashizaki
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 The Institute of Physical and Chemical Research (RIKEN)
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 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
 Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
 Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
 Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
 Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
 Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
 Hayashizaki,Y. Direct Submission
 Computational Analysis of Full-length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.

FEATURES

source
 location/Qualifiers
 1. .329
 /organism="Mus musculus"
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 /db_xref="taxon:10090"
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 whole body"

ORIGIN

Query Match 81.6%; Score 20.4; DB 5; Length 299;
 Best Local Similarity 76.0%; Pred. No. 63;
 Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTYYKTRTACNAGTSG 25

Db 246 GTTCAGCTTTTATAGTGG 270

RESULT 7
 BP757615/c 306 bp mRNA linear EST 08-JUL-2004
 LOCUS
 DEFINITION BP757615 mouse (C57BL/6) pancreatic islet library with
 recombination-based method Mus musculus cDNA clone mib04031 3',
 mRNA sequence.

ACCESSION BP757615.1 GI:50077505

VERSION BP757615

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 306)

Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,

Takeda,J., Ohara,O. and Seino,S.

TITLE Construction of a multi-functional cDNA library specific for mouse

pancreatic islets and its application to microarray

JOURNAL Unpublished (2004)

COMMENT Contact: Susumu Seino

Division of Cellular and Molecular Medicine

Kobe University Graduate School of Medicine
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 Tel: 81-78-382-5360
 Fax: 81-78-382-5370
 Email: seino@med.kobe-u.ac.jp.

FEATURES

source
 location/Qualifiers
 1. .306
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 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="mib04031"
 /sex="male"
 /tissue_type="pancreatic islet"
 /dev_stage="adult"
 /clone_lib="mouse (C57BL/6) pancreatic islet library with
 recombination-based method"

ORIGIN

Query Match 81.6%; Score 20.4; DB 5; Length 306;
 Best Local Similarity 76.0%; Pred. No. 64;
 Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTYYKTRTACNAGTSG 25

Db 109 GTTCAGCTTTTGTACAAAGTTGG 85

RESULT 8

BP754432/c

LOCUS

DEFINITION

BP754432 mouse (C57BL/6) pancreatic islet library with
 recombination-based method Mus musculus cDNA clone mial0061 3',
 mRNA sequence.

ACCESSION BP754432

VERSION BP754432.1 GI:50074322

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 374)

Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,

Takeda,J., Ohara,O. and Seino,S.

TITLE Construction of a multi-functional cDNA library specific for mouse

pancreatic islets and its application to microarray

JOURNAL Unpublished (2004)

COMMENT Contact: Susumu Seino

Division of Cellular and Molecular Medicine

Kobe University Graduate School of Medicine

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Tel: 81-78-382-5360

Fax: 81-78-382-5370

Email: seino@med.kobe-u.ac.jp.

FEATURES

source

location/Qualifiers

1. .374

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/strain="C57BL/6"

/db_xref="taxon:10090"

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/sex="male"

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/clone_lib="mouse (C57BL/6) pancreatic islet library with

recombination-based method"

ORIGIN

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 Best Local Similarity 76.0%; Pred. No. 65;
 Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTYYKTRTACNAGTSG 25


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|||||
73 GTTCAGCTTTTGTACAAAGTTGG 49

Db
RESULT 9
BP754410/c
LOCUS
DEFINITION BP754410 mouse (C57BL/6) pancreatic islet library with
recombination-based method Mus musculus cDNA clone mial0045 3',
mRNA sequence.
ACCESSION BP754410
VERSION BP754410.1 GI:50074300
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 401)
AUTHORS Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
Takeda,J., Ohara,O. and Seino,S.
TITLE Construction of a multi-functional cDNA library specific for mouse
pancreatic islets and its application to microarray
JOURNAL Unpublished (2004)
COMMENT Contact: Susumu Seino
Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.
Location/Qualifiers
1. .401
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/db_xref="taxon:10090"
/clone="mial0045"
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/tissue_type="pancratic islet"
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FEATURES
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recombination-based method"

ORIGIN
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Best Local Similarity 76.0%; Pred. No. 66;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTSCB 25
|||||
Db 52 GTTCAGCTTTTGTACAAAGTTGG 28

RESULT 11
BP754464/c
LOCUS
DEFINITION BP754464 mouse (C57BL/6) pancreatic islet library with
recombination-based method Mus musculus cDNA clone mial0085 3',
mRNA sequence.
ACCESSION BP754464
VERSION BP754464.1 GI:50074354
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 422)
AUTHORS Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
Takeda,J., Ohara,O. and Seino,S.
TITLE Construction of a multi-functional cDNA library specific for mouse
pancreatic islets and its application to microarray
JOURNAL Unpublished (2004)
COMMENT Contact: Susumu Seino
Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.
Location/Qualifiers
1. .422
/organism="Mus musculus"
/mol_type="mRNA"
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/clone="mial0085"
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FEATURES
source
1. .422
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recombination-based method"

ORIGIN
Query Match 81.6%; Score 20.4; DB 5; Length 422;
Best Local Similarity 76.0%; Pred. No. 66;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTSCB 25
|||||
Db 73 GTTCAGCTTTTGTACAAAGTTGG 49

RESULT 10
BP754552/c
LOCUS
DEFINITION BP754552 mouse (C57BL/6) pancreatic islet library with
recombination-based method Mus musculus cDNA clone mial1051 3',
mRNA sequence.
ACCESSION BP754552
VERSION BP754552.1 GI:50074442
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 409)
AUTHORS Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
Takeda,J., Ohara,O. and Seino,S.
TITLE Construction of a multi-functional cDNA library specific for mouse
pancreatic islets and its application to microarray
JOURNAL Unpublished (2004)
COMMENT Contact: Susumu Seino

```

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QY 1 GTTCAGCTTTTKRTACNAAGTSG 25
Db 73 GTTCAGCTTTTGTACAAAGTTGG 49

RESULT 12
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LOCUS BP754551.1 GI:50074441
DEFINITION BP754551 mouse (C57BL/6) pancreatic islet library with
recombination-based method Mus musculus cDNA clone mial1050 3',
mRNA sequence.
ACCESSION BP754551
VERSION BP754551.1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 423)
AUTHORS Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
Takeda,J., Ohara,O. and Seino,S.
TITLE Construction of a multi-functional cDNA library specific for mouse
pancreatic islets and its application to microarray
JOURNAL Unpublished (2004)
COMMENT Contact: Susumu Seino
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Kobe University Graduate School of Medicine
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Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.
Location/Qualifiers
1..423
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recombination-based method"

FEATURES
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Best Local Similarity 76.0%; Pred. No. 66;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

ORIGIN
1 GTTCAGCTTTTKRTACNAAGTSG 25
|||||:::|||||:
73 GTTCAGCTTTTGTACAAAGTTGG 49

RESULT 14
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LOCUS BP754563.1 GI:50074453
DEFINITION BP754563 mouse (C57BL/6) pancreatic islet library with
recombination-based method Mus musculus cDNA clone mial1058 3',
mRNA sequence.
ACCESSION BP754563
VERSION BP754563.1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 432)
AUTHORS Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
Takeda,J., Ohara,O. and Seino,S.
TITLE Construction of a multi-functional cDNA library specific for mouse
pancreatic islets and its application to microarray
JOURNAL Unpublished (2004)
COMMENT Contact: Susumu Seino
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Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.
Location/Qualifiers
1..432
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/mol_type="mRNA"
/strain="C57BL/6"
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/dev_stage="adult"
/clone_lib="mouse (C57BL/6) pancreatic islet library with
recombination-based method"

FEATURES
source
Query Match 81.6%; Score 20.4; DB 5; Length 432;
Best Local Similarity 76.0%; Pred. No. 67;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

ORIGIN
1 GTTCAGCTTTTKRTACNAAGTSG 25
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73 GTTCAGCTTTTGTACAAAGTTGG 49

RESULT 13
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LOCUS BP754589.1 GI:50074479
DEFINITION BP754589 mouse (C57BL/6) pancreatic islet library with
recombination-based method Mus musculus cDNA clone mial1079 3',
mRNA sequence.
ACCESSION BP754589
VERSION BP754589.1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 430)
AUTHORS Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
Takeda,J., Ohara,O. and Seino,S.
TITLE Construction of a multi-functional cDNA library specific for mouse
pancreatic islets and its application to microarray
JOURNAL Unpublished (2004)
COMMENT Contact: Susumu Seino
Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.
Location/Qualifiers
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/strain="C57BL/6"
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/clone="mial1079"
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recombination-based method"

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source
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Best Local Similarity 76.0%; Pred. No. 66;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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73 GTTCAGCTTTTGTACAAAGTTGG 49

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Db 73 GTTCAGCTTTTGTACAAAGTTGG 49

RESULT 15
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LOCUS BP754508 mouse (C57BL/6) pancreatic islet library with
DEFINITION recombination-based method Mus musculus cDNA clone mial1021 3',
mRNA sequence.
BP754508
BP754508.1 GI:50074398
EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 443)
Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
Takeda,J., Ohara,O. and Seino,S.
TITLE Construction of a multi-functional cDNA library specific for mouse
pancreatic islets and its application to microarray
JOURNAL Unpublished (2004)
COMMENT Contact: Susumu Seino
Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.

FEATURES
source
1..443
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recombination-based method"

ORIGIN
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Best Local Similarity 76.0%; Pred. No. 67;
Matches 19; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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Search completed: November 16, 2004, 10:16:34
Job time : 1534 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:29:43 ; Search time 708.5 Seconds
(without alignments)
1668.656 Million cell updates/sec

Title: US-10-820-133-39
Perfect score: 25
Sequence: 1 rbycwgctttrttacwaaastkgd 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

RESULT 1
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LOCUS AR124526 25 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 6 from patent US 6171861.
ACCESSION AR124526
VERSION AR124526.1 GI:14109887
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6171861-A 6 09-JAN-2001;
FEATURES Location/Qualifiers
source 1..25
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/mol_type="unassigned DNA"

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	20.2	80.8	25	6	AR124527 Sequence
3	20.2	80.8	25	6	AR124528 Sequence
4	20.2	80.8	25	6	AR124529 Sequence
5	20.2	80.8	25	6	AR124530 Sequence
6	20.2	80.8	25	6	AR124531 Sequence
7	20.2	80.8	25	6	AR124532 Sequence
8	20.2	80.8	25	6	AR124533 Sequence
9	20.2	80.8	25	6	AR124534 Sequence
10	20.2	80.8	25	6	AR124535 Sequence
11	20.2	80.8	25	6	AR124536 Sequence
12	20.2	80.8	25	6	AR124551 Sequence
13	20.2	80.8	25	6	AR124552 Sequence
14	20.2	80.8	25	6	AR124553 Sequence
15	20.2	80.8	25	6	AR124554 Sequence
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17	20.2	80.8	25	6	AR163177 Sequence
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19	20.2	80.8	25	6	AR163179 Sequence

20	20.2	80.8	25	6	AR163180 Sequence
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23	20.2	80.8	25	6	AR163183 Sequence
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26	20.2	80.8	25	6	AR163186 Sequence
27	20.2	80.8	25	6	AR163187 Sequence
28	20.2	80.8	25	6	AR163202 Sequence
c 29	20.2	80.8	25	6	AR163203 Sequence
c 30	20.2	80.8	25	6	AR163204 Sequence
c 31	20.2	80.8	25	6	AR163205 Sequence
c 32	20.2	80.8	25	6	AR163206 Sequence
c 33	20.2	80.8	25	6	BD263223 Compositi
c 34	20.2	80.8	25	6	BD263224 Compositi
c 35	20.2	80.8	25	6	BD263313 Compositi
c 36	20.2	80.8	25	6	AR493778 Sequence
37	20.2	80.8	25	6	AR493779 Sequence
38	20.2	80.8	25	6	AR493780 Sequence
39	20.2	80.8	25	6	AR493781 Sequence
40	20.2	80.8	25	6	AR493782 Sequence
41	20.2	80.8	25	6	AR493783 Sequence
42	20.2	80.8	25	6	AR493784 Sequence
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Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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DEFINITION Sequence 7 from patent US 6171861.
ACCESSION AR124527
VERSION AR124527.1 GI:14109888
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites

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JOURNAL Patent: US 6171861-A 7 09-JAN-2001;
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LOCUS AR124528 25 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 8 from patent US 6171861.
ACCESSION AR124528
VERSION AR124528.1 GI:14109889
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  AUTHORS Hartley,J.L. and Brasch,M.A.
  TITLE Recombinational cloning using engineered recombination sites
  JOURNAL Patent: US 6171861-A 8 09-JAN-2001;
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LOCUS AR124529 25 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 9 from patent US 6171861.
ACCESSION AR124529
VERSION AR124529.1 GI:14109890
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  AUTHORS Hartley,J.L. and Brasch,M.A.
  TITLE Recombinational cloning using engineered recombination sites
  JOURNAL Patent: US 6171861-A 9 09-JAN-2001;
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LOCUS AR124530 25 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 10 from patent US 6171861.
ACCESSION AR124530
VERSION AR124530.1 GI:14109891
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  AUTHORS Hartley,J.L. and Brasch,M.A.
  TITLE Recombinational cloning using engineered recombination sites
  JOURNAL Patent: US 6171861-A 10 09-JAN-2001;
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LOCUS AR124531 25 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 11 from patent US 6171861.
ACCESSION AR124531
VERSION AR124531.1 GI:14109892
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  AUTHORS Hartley,J.L. and Brasch,M.A.
  TITLE Recombinational cloning using engineered recombination sites
  JOURNAL Patent: US 6171861-A 11 09-JAN-2001;
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RESULT 7
AR124532
LOCUS AR124532 25 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 12 from patent US 6171861.
ACCESSION AR124532
VERSION AR124532.1 GI:14109893
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  AUTHORS Hartley,J.L. and Brasch,M.A.
  TITLE Recombinational cloning using engineered recombination sites
  JOURNAL Patent: US 6171861-A 12 09-JAN-2001;
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RESULT 13
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VERSION     ARI124552.1 GI:14109913
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 25)
AUTHORS    Hartley,J.L. and Brasch,M.A.
TITLE       Recombinational cloning using engineered recombination sites
JOURNAL     Patent: US 6171861-A 32 09-JAN-2001;
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QY      1  RBYCWGCTTTTTRTACAAATRGD 25
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RESULT 15

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:29:13 ; Search time 167.8 Seconds
(without alignments)
782.095 Million cell updates/sec

Title: US-10-820-133-39
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Gapop 10.0 , Gapext 1.0

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001as.*
5: Geneseq2001bs.*
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7: Geneseq2002bs.*
8: Geneseq2003as.*
9: Geneseq2003bs.*
10: Geneseq2003cs.*
11: Geneseq2003ds.*
12: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	20.2	80.8	25	2	AAT48221 attL1 cor
5	20.2	80.8	25	2	AAT48219 attR2 cor
6	20.2	80.8	25	2	AAT48222 attL2 cor
7	20.2	80.8	25	2	AAT48223 attL3 cor
8	20.2	80.8	25	2	AAT48224 attP1 cor
9	20.2	80.8	25	2	AAT48218 attR1 cor
10	20.2	80.8	25	2	AAT48217 attB3 cor
11	20.2	80.8	25	2	AAX78973 Oligonucl
12	20.2	80.8	25	2	AAX78994 Oligonucl
13	20.2	80.8	25	2	AAX78977 Oligonucl
14	20.2	80.8	25	2	AAX78940 Oligonucl
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25	20.2	80.8	25	2	AAX78943 Oligonucl
26	20.2	80.8	25	2	AAX78946 Oligonucl
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ALIGNMENTS

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DT 20-OCT-1997 (first entry)
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KW att recombination site; core region; mutation; enhance; recombination;
KW vector; subcloning; regulation; exchange; ss.
XX
OS Synthetic.
XX
PN WO9640724-A1.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US010082.
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PR 07-JUN-1995; 95US-00486139.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Hartley JL, Brasch MA;
XX
DR WPI; 1997-065168/06.
XX
PT Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
PT using recombinant proteins and engineered recombination sites in vitro or
PT in vivo.
XX
PS Claim 14; Page 55; 106pp; English.
XX
CC AAT48210-25 are att recombination site core region DNA sequences. The
CC core region has at least one engineered mutation that enhances
CC recombination in vitro in the formation of a Cointegrate or Product DNA.
CC These core regions can be incorporated into novel vector donor DNA
CC molecules. The nucleic acids, vectors and methods of the invention are
CC used to obtain chimeric nucleic acid using recombination proteins and
CC engineered recombination sites in vitro or in vivo. The improved
CC specificity, speed and yields of the invention facilitates DNA or RNA
CC subcloning, regulation or exchange useful for any related purpose, e.g.

CC	in vitro recombination of DNA segments, and in vitro or in vivo insertion
CC	or modification of transcribed, replicated, isolated or genomic DNA or
CC	RNA
XX	
SQ	Sequence 25 BP; 5 A; 6 C; 4 G; 10 T; 0 U; 0 Other;
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	Best Local Similarity 60.0%; Pred.No.28;
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Db	1 AGCCTGCTTCTGTACAACACTTG 25 ::: :: :: :: :: :: :
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DT	20-OCT-1997 (first entry)
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DE	attP2.P3 core region.
XX	
KW	att recombination site; core region; mutation; enhance; recombination;
KW	vector; subcloning; regulation; exchange; gs.
OS	Synthetic.
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FN	WO9640724-A1.
PD	19-DEC-1996.
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PF	07-JUN-1996; 96WO-US010082.
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FR	07-JUN-1995; 95US-00486139.
XX	
PA	(LIFE-) LIFE TECHNOLOGIES INC.
XX	
PI	Hartley JL, Braesch MA;
XX	
DR	WPI; 1997-065168/06.
XX	
PT	Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
PT	using recombinant proteins and engineered recombination sites in vitro or
PT	in vivo.
XX	
PS	Claim 14; Page 56; 106pp; English.
XX	
CC	AAT48210-25 are att recombination site core region DNA sequences. The
CC	core region has at least one engineered mutation that enhances
CC	recombination in vitro in the formation of a Cointegrate or Product DNA.
CC	These core regions can be incorporated into novel vector donor DNA
CC	molecules. The nucleic acids, vectors and methods of the invention are
CC	used to obtain chimeric nucleic acid using recombination proteins and
CC	engineered recombination sites in vitro or in vivo. The improved
CC	specificity, speed and yields of the invention facilitates DNA or RNA
CC	subcloning, regulation or exchange useful for any related purpose, e.g.
CC	in vitro recombination of DNA segments, and in vitro or in vivo insertion
CC	or modification of transcribed, replicated, isolated or genomic DNA or
CC	RNA
XX	
SQ	Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 U; 0 Other;
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	Best Local Similarity 60.0%; Pred.No.28;
	Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;
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Db	1 GTTCAGCTTCTGTACAAGAATTGG 25 ::: :: :: :: :: :: :

CC engineered recombination sites in vitro or in vivo. The improved
 CC specificity, speed and yields of the invention facilitates DNA or RNA
 CC subcloning, regulation or exchange useful for any related purpose, e.g.
 CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
 CC or modification of transcribed, replicated, isolated or genomic DNA or
 CC RNA

SQ Sequence 25 BP; 5 A; 5 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 80.8%; Score 20.2; DB 2; Length 25;
 Best Local Similarity 60.0%; Pred. No. 28;
 Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 1 RBYCWGCTTTTTRTACWAASTKGD 25

Db 1 AGCGTGCTTTCTGTACAAAGTTGG 25

RESULT 7

AAT48223

ID AAT48223 standard; DNA; 25 BP.

XX AC AAT48223;

DT 20-OCT-1997 (first entry)

DE attL3 core region.

XX att recombination site; core region; mutation; enhance; recombination;
 KW vector; subcloning; regulation; exchange; ss.

XX Synthetic.

XX WO9640724-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US010082.

XX 07-JUN-1995; 95US-00486139.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA;

XX WPI; 1997-065168/06.

XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
 PT using recombinant proteins and engineered recombination sites in vitro or
 PT in vivo.

PS Claim 14; Page 56; 106pp; English.

XX AAT48210-25 are att recombination site core region DNA sequences. The
 CC core region has at least one engineered mutation that enhances
 CC recombination in vitro in the formation of a Cointegrate or Product DNA.
 CC These core regions can be incorporated into novel vector donor DNA
 CC molecules. The nucleic acids, vectors and methods of the invention are
 CC used to obtain chimeric nucleic acid using recombination proteins and
 CC engineered recombination sites in vitro or in vivo. The improved
 CC specificity, speed and yields of the invention facilitates DNA or RNA
 CC subcloning, regulation or exchange useful for any related purpose, e.g.
 CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
 CC or modification of transcribed, replicated, isolated or genomic DNA or
 CC RNA

SQ Sequence 25 BP; 6 A; 6 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 80.8%; Score 20.2; DB 2; Length 25;
 Best Local Similarity 60.0%; Pred. No. 28;
 Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 1 RBYCWGCTTTTTRTACWAASTKGD 25

Db 1 ACCCAGCTTTCTGTACAAAGTTGG 25

RESULT 8

AAT48224

ID AAT48224 standard; DNA; 25 BP.

XX AC AAT48224;

DT 20-OCT-1997 (first entry)

DE attP1 core region.

XX att recombination site; core region; mutation; enhance; recombination;
 KW vector; subcloning; regulation; exchange; ss.

XX Synthetic.

XX WO9640724-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US010082.

XX 07-JUN-1995; 95US-00486139.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA;

XX WPI; 1997-065168/06.

XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
 PT using recombinant proteins and engineered recombination sites in vitro or
 PT in vivo.

PS Claim 14; Page 56; 106pp; English.

XX AAT48210-25 are att recombination site core region DNA sequences. The
 CC core region has at least one engineered mutation that enhances
 CC recombination in vitro in the formation of a Cointegrate or Product DNA.
 CC These core regions can be incorporated into novel vector donor DNA
 CC molecules. The nucleic acids, vectors and methods of the invention are
 CC used to obtain chimeric nucleic acid using recombination proteins and
 CC engineered recombination sites in vitro or in vivo. The improved
 CC specificity, speed and yields of the invention facilitates DNA or RNA
 CC subcloning, regulation or exchange useful for any related purpose, e.g.
 CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
 CC or modification of transcribed, replicated, isolated or genomic DNA or
 CC RNA

SQ Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 U; 0 Other;

Query Match 80.8%; Score 20.2; DB 2; Length 25;
 Best Local Similarity 60.0%; Pred. No. 28;
 Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 1 RBYCWGCTTTTTRTACWAASTKGD 25

Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 9

AAT48218

ID AAT48218 standard; DNA; 25 BP.

XX AC AAT48218;

DT 20-OCT-1997 (first entry)

DE attR1 core region.

KW att recombination site; core region; mutation; enhance; recombination;
 KW vector; subcloning; regulation; exchange; ss.
 XX Synthetic.
 OS WO9640724-A1.
 PN 19-DEC-1996.
 PD
 XX 07-JUN-1996; 96WO-US010082.
 XX 07-JUN-1995; 95US-00486139.
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 XX Hartley JL, Brasch MA;
 XX WPI; 1997-065168/06.
 XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
 PT using recombinant proteins and engineered recombination sites in vitro or
 PT in vivo.
 XX Claim 14; Page 55; 106pp; English.
 XX AAT48210-25 are att recombination site core region DNA sequences. The
 CC core region has at least one engineered mutation that enhances
 CC recombination in vitro in the formation of a CoIntegrate or Product DNA.
 CC These core regions can be incorporated into novel vector donor DNA
 CC molecules. The nucleic acids, vectors and methods of the invention are
 CC used to obtain chimeric nucleic acid using recombination proteins and
 CC engineered recombination sites in vitro or in vivo. The improved
 CC specificity, speed and yields of the invention facilitates DNA or RNA
 CC subcloning, regulation or exchange useful for any related purpose, e.g.
 CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
 CC or modification of transcribed, replicated, isolated or genomic DNA or
 CC RNA
 XX Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 U; 0 Other;
 XX
 XX Query Match 80.8%; Score 20.2; DB 2; Length 25;
 XX Best Local Similarity 60.0%; Pred. No. 28;
 XX Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RBVCWGCTTTTTRTACWAASTKGD 25
 Db :::::|||||:|||||:|||||:|||||:
 1 GTTCAGCTTTTGTGACAACTTGT 25
 RESULT 10
 AAT48217
 ID AAT48217 standard; DNA; 25 BP.
 XX
 XX AC AAT48217;
 XX 20-OCT-1997 (first entry)
 DT attB3 core region.
 DE
 XX att recombination site; core region; mutation; enhance; recombination;
 KW vector; subcloning; regulation; exchange; ss.
 XX Synthetic.
 OS WO9640724-A1.
 PN 19-DEC-1996.
 PD
 XX 07-JUN-1996; 96WO-US010082.
 XX 07-JUN-1995; 95US-00486139.
 XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA;
 XX WPI; 1997-065168/06.
 XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
 PT using recombinant proteins and engineered recombination sites in vitro or
 PT in vivo.
 XX Claim 14; Page 55; 106pp; English.
 XX AAT48210-25 are att recombination site core region DNA sequences. The
 CC core region has at least one engineered mutation that enhances
 CC recombination in vitro in the formation of a CoIntegrate or Product DNA.
 CC These core regions can be incorporated into novel vector donor DNA
 CC molecules. The nucleic acids, vectors and methods of the invention are
 CC used to obtain chimeric nucleic acid using recombination proteins and
 CC engineered recombination sites in vitro or in vivo. The improved
 CC specificity, speed and yields of the invention facilitates DNA or RNA
 CC subcloning, regulation or exchange useful for any related purpose, e.g.
 CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
 CC or modification of transcribed, replicated, isolated or genomic DNA or
 CC RNA
 XX Sequence 25 BP; 6 A; 7 C; 3 G; 9 T; 0 U; 0 Other;
 XX
 XX Query Match 80.8%; Score 20.2; DB 2; Length 25;
 XX Best Local Similarity 60.0%; Pred. No. 28;
 XX Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RBVCWGCTTTTTRTACWAASTKGD 25
 Db :::::|||||:|||||:|||||:|||||:
 1 ACCCAGCTTTCTGTGACAACTTGT 25
 RESULT 11
 AAX78973
 ID AAX78973 standard; DNA; 25 BP.
 XX
 XX AC AAX78973;
 XX 17-AUG-1999 (first entry)
 DT Oligonucleotide #39 for recombination and cloning method.
 DE Cloning; donor; recombination site; vector; chimeric; ss.
 XX
 XX OS Synthetic.
 XX WO9921977-A1.
 PN 06-MAY-1999.
 PD
 XX 26-OCT-1998; 98WO-US022589.
 XX 24-OCT-1997; 97US-0065930P.
 PR 23-OCT-1998; 98US-00177387.
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 XX Hartley JL, Brasch MA, Temple GF, Fox DK;
 XX WPI; 1999-303011/25.
 XX New nucleic acid cloning methods.
 XX Disclosure; Page 169; 185pp; English.
 XX The invention relates to novel methods for cloning or subcloning one or
 CC more nucleic acid molecules (NAs) comprising: (a) combining in vitro or
 CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
 CC more desired nucleic acid segments flanked by at least 2 recombination
 CC sites which do not recombine with each other; (2) one or more vector

CC donor molecules (VDMs) comprising at least 2 recombination sites which do
CC not recombine with each other; and (3) one or more site-specific
CC recombination proteins; (b) incubating the combination to transfer one or
CC more of the desired segments into one or more of the VDMs, thereby
CC producing one or more desired product molecules (PMS). The methods can be
CC used for the efficient and specific recombination of NAM segments. They
CC can be used to generate chimeric DNA or RNA molecules that have the
CC desired characteristics and/or nucleic acid segments. The methods can
CC also be used for changing vectors. The oligonucleotides AAX78935-X78994
CC are used in the method of the invention

XX Sequence 25 BP; 3 A; 3 C; 2 G; 7 T; 0 U; 10 Other;

Query Match 80.8%; Score 20.2; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25
Db 1 RBYCWGCTTTTTRTACWAASTKGD 25

RESULT 12

AAX78994
ID AAX78994 standard; DNA; 25 BP.

AC AAX78994;

DT 17-AUG-1999 (first entry)

XX Oligonucleotide #60 for recombination and cloning method.

DE Cloning; donor; recombination site; vector; chimeric; ss.

KW Synthetic.

OS Synthetic.

XX WO9921977-A1.

PN 06-MAY-1999.

XX 26-OCT-1998; 98WO-US022589.

XX 24-OCT-1997; 97US-0065930P.

PR 23-OCT-1998; 98US-00177387.

XX (LIFE-) LIFE TECHNOLOGIES INC.
XX Hartley JL, Brasch MA, Temple GF, Fox DK;
XX WPI; 1999-303011/25.

XX New nucleic acid cloning methods.

XX Disclosure; Page 176; 185pp; English.

XX The invention relates to novel methods for cloning or subcloning one or
XX more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
XX in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
XX more desired nucleic acid segments flanked by at least 2 recombination
XX sites which do not recombine with each other; (2) one or more vector
XX donor molecules (VDMs) comprising at least 2 recombination sites which
XX do not recombine with each other; and (3) one or more site-specific
XX recombination proteins; (b) incubating the combination to transfer one or
XX more of the desired segments into one or more of the VDMs, thereby
XX producing one or more desired product molecules (PMS). The methods can be
XX used for the efficient and specific recombination of NAM segments. They
XX can be used to generate chimeric DNA or RNA molecules that have the
XX desired characteristics and/or nucleic acid segments. The methods can
XX also be used for changing vectors. The oligonucleotides AAX78935-X78994
XX are used in the method of the invention

XX Sequence 25 BP; 6 A; 5 C; 3 G; 11 T; 0 U; 0 Other;

Query Match 80.8%; Score 20.2; DB 2; Length 25;
Best Local Similarity 60.0%; Pred. No. 28;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25
Db 1 AGCCTGCTTTTATACAACTTGA 25

RESULT 13

AAX78977
ID AAX78977 standard; DNA; 25 BP.

XX AAX78977;

XX 17-AUG-1999 (first entry)

XX Oligonucleotide #43 for recombination and cloning method.

DE Cloning; donor; recombination site; vector; chimeric; ss.

KW Synthetic.

XX WO9921977-A1.

XX 06-MAY-1999.

XX 26-OCT-1998; 98WO-US022589.

XX 24-OCT-1997; 97US-0065930P.

PR 23-OCT-1998; 98US-00177387.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Fox DK;
XX WPI; 1999-303011/25.

XX New nucleic acid cloning methods.

XX Disclosure; Page 171; 185pp; English.

XX The invention relates to novel methods for cloning or subcloning one or
XX more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
XX in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
XX more desired nucleic acid segments flanked by at least 2 recombination
XX sites which do not recombine with each other; (2) one or more vector
XX donor molecules (VDMs) comprising at least 2 recombination sites which do
XX not recombine with each other; and (3) one or more site-specific
XX recombination proteins; (b) incubating the combination to transfer one or
XX more of the desired segments into one or more of the VDMs, thereby
XX producing one or more desired product molecules (PMS). The methods can be
XX used for the efficient and specific recombination of NAM segments. They
XX can be used to generate chimeric DNA or RNA molecules that have the
XX desired characteristics and/or nucleic acid segments. The methods can
XX also be used for changing vectors. The oligonucleotides AAX78935-X78994
XX are used in the method of the invention

XX Sequence 25 BP; 4 A; 3 C; 5 G; 10 T; 0 U; 3 Other;

Query Match 80.8%; Score 20.2; DB 2; Length 25;
Best Local Similarity 72.0%; Pred. No. 28;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25
Db 1 GTTCAGCTTTTTRTACWAAAGTTGG 25

RESULT 14

AAX78940
ID AAX78940 standard; DNA; 25 BP.

XX

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:19 ; Search time 35.9 Seconds
(without alignments)
494.978 Million cell updates/sec

Title: US-10-820-133-39

Perfect score: 25

Sequence: 1 rbycggtttrttacwaastkgd 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
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6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	20.2	80.8	25	3	US-09-233-493-7
3	20.2	80.8	25	3	US-09-233-493-8
4	20.2	80.8	25	3	US-09-233-493-9
5	20.2	80.8	25	3	US-09-233-493-10
6	20.2	80.8	25	3	US-09-233-493-11
7	20.2	80.8	25	3	US-09-233-493-12
8	20.2	80.8	25	3	US-09-233-493-13
9	20.2	80.8	25	3	US-09-233-493-14
10	20.2	80.8	25	3	US-09-233-493-15
11	20.2	80.8	25	3	US-09-233-493-16
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14	20.2	80.8	25	3	US-09-233-493-33
15	20.2	80.8	25	3	US-09-233-493-34
16	20.2	80.8	25	3	US-09-233-493-35
17	20.2	80.8	25	3	US-09-005-476-6
18	20.2	80.8	25	3	US-09-005-476-7
19	20.2	80.8	25	3	US-09-005-476-8
20	20.2	80.8	25	3	US-09-005-476-9
21	20.2	80.8	25	3	US-09-005-476-10
22	20.2	80.8	25	3	US-09-005-476-11
23	20.2	80.8	25	3	US-09-005-476-12
24	20.2	80.8	25	3	US-09-005-476-13
25	20.2	80.8	25	3	US-09-005-476-14
26	20.2	80.8	25	3	US-09-005-476-15
27	20.2	80.8	25	3	US-09-005-476-16

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Sequence 32, Appl
Sequence 33, Appl
Sequence 34, Appl
Sequence 35, Appl
Sequence 6, Appl
Sequence 7, Appl
Sequence 8, Appl
Sequence 9, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 31, Appl
Sequence 32, Appl

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36 20.2 80.8 25 3 US-09-233-492-9
37 20.2 80.8 25 3 US-09-233-492-10
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43 20.2 80.8 25 3 US-09-233-492-16
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c 45 20.2 80.8 25 3 US-09-233-492-32

ALIGNMENTS

RESULT 1
US-09-233-493-6
; Sequence 6, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
US-09-233-493-6

Query Match 80.8%; Score 20.2; DB 3; Length 25;
 Best Local Similarity 60.0%; Pred. No. 4.5;
 Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBVCGCTTTTTRTACWAATKGD 25
 Db 1 AGCCTGCTTTTGTGACAACTTGT 25

RESULT 2

US-09-233-493-7
 ; Sequence 7, Application US/09233493
 ; Patent No. 6143557
 ; GENERAL INFORMATION:
 ; APPLICANT: Hartley, James L.
 ; APPLICANT: Brasch, Michael A.
 ; TITLE OF INVENTION: Recombinational Cloning Using Engineered
 ; TITLE OF INVENTION: Recombination Sites
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
 ; STREET: 1100 New York Ave., N. W. Suite 600
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/233,493

FILING DATE: 20-JAN-1999

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/005,476

FILING DATE: 12-JAN-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/663,002

FILING DATE: 07-JUN-1996

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/486,139

FILING DATE: 07-JUN-1995

CLASSIFICATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: CDNA

US-09-233-493-7

Query Match 80.8%; Score 20.2; DB 3; Length 25;
 Best Local Similarity 60.0%; Pred. No. 4.5;
 Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBVCGCTTTTTRTACWAATKGD 25
 Db 1 AGCCTGCTTTTGTGACAACTTGT 25

RESULT 3

US-09-233-493-8
 ; Sequence 8, Application US/09233493
 ; Patent No. 6143557
 ; GENERAL INFORMATION:

APPLICANT: Hartley, James L.
 APPLICANT: Brasch, Michael A.
 TITLE OF INVENTION: Recombinational Cloning Using Engineered
 TITLE OF INVENTION: Recombination Sites
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
 STREET: 1100 New York Ave., N. W. Suite 600
 CITY: Washington
 STATE: DC
 COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/233,493

FILING DATE: 20-JAN-1999

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/005,476

FILING DATE: 12-JAN-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/663,002

FILING DATE: 07-JUN-1996

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/486,139

FILING DATE: 07-JUN-1995

CLASSIFICATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: CDNA

US-09-233-493-8

Query Match 80.8%; Score 20.2; DB 3; Length 25;
 Best Local Similarity 60.0%; Pred. No. 4.5;
 Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBVCGCTTTTTRTACWAATKGD 25
 Db 1 ACCGAGCTTCTTGTACAACTTGT 25

RESULT 4

US-09-233-493-9
 ; Sequence 9, Application US/09233493
 ; Patent No. 6143557
 ; GENERAL INFORMATION:

APPLICANT: Hartley, James L.

APPLICANT: Brasch, Michael A.

TITLE OF INVENTION: Recombinational Cloning Using Engineered

TITLE OF INVENTION: Recombination Sites

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C

STREET: 1100 New York Ave., N. W. Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-233-493-9

Query Match      80.8%; Score 20.2; DB 3; Length 25;
Best Local Similarity 60.0%; Pred. No. 4.5;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWCCTTTTTRTACWAASTKGD 25
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Db 1 GTTCAGCTTTTCTGTACAAACTTGT 25

RESULT 5
US-09-233-493-10
; Sequence 10, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-233-493-10

Query Match      80.8%; Score 20.2; DB 3; Length 25;
Best Local Similarity 60.0%; Pred. No. 4.5;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWCCTTTTTRTACWAASTKGD 25
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Db 1 GTTCAGCTTTTCTGTACAAACTTGT 25

RESULT 6
US-09-233-493-11
; Sequence 11, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
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; MOLECULE TYPE: cdna
US-09-233-493-11

Query Match      80.8%; Score 20.2; DB 3; Length 25;
Best Local Similarity 60.0%; Pred. No. 4.5;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTTCAGCTTCTTGTACAAAGTTGG 25

RESULT 7
US-09-233-493-12
; Sequence 12, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; INFORMATION FOR SEQ ID NO: 12:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-493-13

Query Match      80.8%; Score 20.2; DB 3; Length 25;
Best Local Similarity 60.0%; Pred. No. 4.5;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25
   ::::|||||:|||||:|||||:|||||:
Db 1 AGCCTGCTTTTCTGTACAAAGTTGG 25

RESULT 9
US-09-233-493-14
; Sequence 14, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
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ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-493-14

Query Match 80.8%; Score 20.2; DB 3; Length 25;
Best Local Similarity 60.0%; Pred. No. 4.5;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCGCTTTTTRTACMAASTKGD 25
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Db 1 ACCGAGCTTCTGTGACAAAGTTGG 25

RESULT 10
US-09-233-493-15
Sequence 15, Application US/09233493
Patent No. 6143557
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-493-15

Query Match 80.8%; Score 20.2; DB 3; Length 25;
Best Local Similarity 60.0%; Pred. No. 4.5;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCGCTTTTTRTACMAASTKGD 25
:::|||||:|||||:|||||:|||||:
Db 1 GTTCAGCTTTTGTGACAAAGTTGG 25

RESULT 11
US-09-233-493-16
Sequence 16, Application US/09233493
Patent No. 6143557
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs

;
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-493-16

Query Match 80.8%; Score 20.2; DB 3; Length 25;
Best Local Similarity 60.0%; Pred. No. 4.5;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 1 RBYCWGCTTTTTRTACWAASTKGD 25
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Db 1 GTTCAGCTTCTGTACAAAGTTGG 25

RESULT 12

US-09-233-493-31
; Sequence 31, Application US/092333493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-493-31

Query Match 80.8%; Score 20.2; DB 3; Length 25;
Best Local Similarity 60.0%; Pred. No. 4.5;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 1 RBYCWGCTTTTTRTACWAASTKGD 25
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Db 1 AGCCTGCTTTTATATACTAATTGA 25

RESULT 13

US-09-233-493-32/c
; Sequence 32, Application US/092333493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-493-32

Query Match 80.8%; Score 20.2; DB 3; Length 25;
Best Local Similarity 60.0%; Pred. No. 4.5;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 1 RBYCWGCTTTTTRTACWAASTKGD 25
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Db 25 AGCCTGCTTTTATATACTAATTGA 1

RESULT 14

US-09-233-493-33/c
; Sequence 33, Application US/092333493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600

; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; APPLICATION NUMBER: US/09/233.493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-233-493-33

Query Match 80.8%; Score 20.2; DB 3; Length 25;
Best Local Similarity 60.0%; Pred. No. 4.5;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15

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; Sequence 34, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233.493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; US-09-233-493-34

Query Match 80.8%; Score 20.2; DB 3; Length 25;
Best Local Similarity 60.0%; Pred. No. 4.5;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	20.2	80.8	25	9	US-09-732-914-9 Sequence 9, Appli
4	20.2	80.8	25	9	US-09-732-914-12 Sequence 12, Appli
5	20.2	80.8	25	9	US-09-732-914-95 Sequence 95, Appli
6	20.2	80.8	25	9	US-09-855-797A-6 Sequence 6, Appli
7	20.2	80.8	25	9	US-09-855-797A-7 Sequence 7, Appli
8	20.2	80.8	25	9	US-09-855-797A-8 Sequence 8, Appli
9	20.2	80.8	25	9	US-09-855-797A-9 Sequence 9, Appli
10	20.2	80.8	25	9	US-09-855-797A-10 Sequence 10, Appli
11	20.2	80.8	25	9	US-09-855-797A-11 Sequence 11, Appli
12	20.2	80.8	25	9	US-09-855-797A-12 Sequence 12, Appli

13	20.2	80.8	25	9	US-09-855-797A-13 Sequence 13, Appli
14	20.2	80.8	25	9	US-09-855-797A-14 Sequence 14, Appli
15	20.2	80.8	25	9	US-09-855-797A-15 Sequence 15, Appli
16	20.2	80.8	25	9	US-09-855-797A-16 Sequence 16, Appli
17	20.2	80.8	25	9	US-09-855-797A-39 Sequence 39, Appli
18	20.2	80.8	25	9	US-09-855-797A-40 Sequence 40, Appli
19	20.2	80.8	25	9	US-09-855-797A-41 Sequence 41, Appli
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22	20.2	80.8	25	9	US-09-855-797A-60 Sequence 60, Appli
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37	20.2	80.8	25	9	US-09-907-900-16 Sequence 16, Appli
38	20.2	80.8	25	9	US-09-907-900-39 Sequence 39, Appli
39	20.2	80.8	25	9	US-09-907-900-40 Sequence 40, Appli
40	20.2	80.8	25	9	US-09-907-900-41 Sequence 41, Appli
41	20.2	80.8	25	9	US-09-907-900-42 Sequence 42, Appli
42	20.2	80.8	25	9	US-09-907-900-43 Sequence 43, Appli
43	20.2	80.8	25	9	US-09-907-900-60 Sequence 60, Appli
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45	20.2	80.8	25	9	US-09-907-719-7 Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-732-914-5
; Sequence 5, Application US/09732914
; Patent No. US20020007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in
; FILE REFERENCE: 0942.5010002
; CURRENT APPLICATION NUMBER: US/09/732.914
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: DNA
; ORGANISM: attB1
US-09-732-914-5

Query Match 80.8%; Score 20.2; DB 9; Length 25;
Best Local Similarity 60.0%; Pred. No.19;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;
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Db 1 AGCTGCTTTTGTACAACTTGT 25

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RESULT 2
US-09-732-914-8
; Sequence 8, Application US/09732914
; Patent No. US20020007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in
; TITLE OF INVENTION: Recombinational Cloning
; FILE REFERENCE: 0942.5010002
; CURRENT APPLICATION NUMBER: US/09/732,914
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 25
; TYPE: DNA
; ORGANISM: attr1
US-09-732-914-8

Query Match      80.8%; Score 20.2; DB 9; Length 25;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25
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Db 1 GTTCAGCTTTTCTGTACAACTGT 25

RESULT 3
US-09-732-914-9
; Sequence 9, Application US/09732914
; Patent No. US20020007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in
; TITLE OF INVENTION: Recombinational Cloning
; FILE REFERENCE: 0942.5010002
; CURRENT APPLICATION NUMBER: US/09/732,914
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: attr2
US-09-732-914-9

Query Match      80.8%; Score 20.2; DB 9; Length 25;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25
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Db 1 ACCCAGCTTTCTGTACAACTGT 25

RESULT 4
US-09-732-914-12
; Sequence 12, Application US/09732914
; Patent No. US20020007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in
; TITLE OF INVENTION: Recombinational Cloning
; FILE REFERENCE: 0942.5010002
; CURRENT APPLICATION NUMBER: US/09/732,914
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 25
; TYPE: DNA
; ORGANISM: attr2
US-09-732-914-12

Query Match      80.8%; Score 20.2; DB 9; Length 25;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25
   :::::::::::::::::::::
Db 1 GTTCAGCTTTTCTGTACAACTGT 25

RESULT 5
US-09-732-914-95/c
; Sequence 95, Application US/09732914
; Patent No. US20020007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in
; TITLE OF INVENTION: Recombinational Cloning
; FILE REFERENCE: 0942.5010002
; CURRENT APPLICATION NUMBER: US/09/732,914
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 95
; LENGTH: 25
; TYPE: DNA
; ORGANISM: attr0
US-09-732-914-95

Query Match      80.8%; Score 20.2; DB 9; Length 25;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

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Db 25 AGCCTGCTTTTATATACTAAGTTGA 1

RESULT 6
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US-09-855-797A-6
; Sequence 6, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-6

Query Match 80.8%; Score 20.2; DB 9; Length 25;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25
:::|||||:|||||:|||||:|:
Db 1 AGCCTGCTTTTGTGACAACTTGT 25

RESULT 7
US-09-855-797A-7
; Sequence 7, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-7

Query Match 80.8%; Score 20.2; DB 9; Length 25;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AGCCTGCTTTTGTGACAACTTGT 25

RESULT 8
US-09-855-797A-8
; Sequence 8, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
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; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-8

Query Match 80.8%; Score 20.2; DB 9; Length 25;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ACCCAGCTTCTTGTACAAAGTGT 25

RESULT 9
US-09-855-797A-9
; Sequence 9, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
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; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-9

Query Match 80.8%; Score 20.2; DB 9; Length 25;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

ORGANISM: UNKNOWN

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
594.643 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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SUMMARIES

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ALIGNMENTS

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Clone MP1Zp2001P061Q 5-PRIME, mRNA sequence.
ACCESSION
CF651937
VERSION
CF651937.1 GI:37427952
KEYWORDS
EST.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
REFERENCE
1 (bases 1 to 79)
AUTHORS
Schmid, K.J., Soerensen, T.R., Stracke, R., Torjek, O., Altmann, T., Mitchell-Olds, T. and Weishaar, B.
TITLE
Large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
JOURNAL
Genome Res. 13 (6), 1250-1257 (2003)
MEDLINE
22683290
PUBMED
12799357
COMMENT
Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 0049215062851
Email: weishaar@mpiz-koeln.mpg.de
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Location/Qualifiers
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/note="Vector: PCW6SPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from Arabidopsis thaliana, accession
Wassilewskija-0; roots from three weeks old plants grown
on MS-plates at 26M-OC with 16 hours light/day; library
was made at the Max-Planck-Institute for Plant Breeding
Research, Cologne, Germany; cloning sites SalI-NotI,

primer sites and orientation:
 SP6-Sall-CCACGGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; GATEWAY compatible; Note: Sequencing granted in the context of the GABI Arabidopsis Verbund I: Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection' PI: Bernd Weishaar Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de> This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further information."

ORIGIN

Query Match 80.8%; Score 20.2; DB 7; Length 79;
 Best Local Similarity 60.0%; Pred. No. 2.2e+02;
 Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25
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 Db 48 ACCCAGCTTCTTGTCACAAAGTGGT 72

RESULT 2

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 LOCUS CB394681
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 EST
 SOURCE
 ORGANISM

Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

REFERENCE

1 (bases 1 to 80)
 Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S., Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Tolias,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H., Doucette-Stamm,L., Hill,D.E. and Vidal,M.
 C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression

TITLE

C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression

JOURNAL

Nat. Genet. (2003) In press

COMMENT

Contact: Vidal M
 Marc Vidal Laboratory
 Dana Farber Cancer Institute
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
 Tel: 617 632 5180
 Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu
 POLYA=No.

FEATURES

source

1. 80

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/mol_type="mRNA"

/strain="N2"

/db_xref="taxon:6239"

/sex="Hermaphrodite and male"

/tissue_type="whole animal"

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/clone_lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

ORIGIN

Query Match 80.8%; Score 20.2; DB 6; Length 80;

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 Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25
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 Db 55 ACCCAGCTTCTTGTCACAAAGTGGT 31

RESULT 3

CB398074

LOCUS CB398074 83 bp mRNA linear EST 15-MAY-2003
 DEFINITION OSTR197D3_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
 ACCESSION CB398074
 VERSION CB398074.1 GI:30739801

KEYWORDS

EST

SOURCE

ORGANISM

Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

REFERENCE

1 (bases 1 to 83)

Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S., Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Tolias,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H., Doucette-Stamm,L., Hill,D.E. and Vidal,M.

C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression

Nat. Genet. (2003) In press

Contact: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu
 POLYA=No.

FEATURES

Location/Qualifiers

1. 83

/organism="Caenorhabditis elegans"

/mol_type="mRNA"

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/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

ORIGIN

Query Match 80.8%; Score 20.2; DB 6; Length 83;
 Best Local Similarity 60.0%; Pred. No. 2.2e+02;
 Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25
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 Db 33 AGCCTGCTTTTCTTGTCACAACTTGT 57

RESULT 4

CB401650/c

LOCUS CB401650 83 bp mRNA linear EST 15-MAY-2003
 DEFINITION OSTR197D3_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
 ACCESSION CB401650


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VERSION      CB401650.1  GI:30743377
KEYWORDS     EST.
SOURCE       Caenorhabditis elegans
ORGANISM     Caenorhabditis elegans
REFERENCE    Rhabditoidea; Metazoa; Chromadorea; Rhabditida;
AUTHORS      1 (bases 1 to 83)
              Rebol,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M.,
              Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T.,
              Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
              Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V.,
              Tolias,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
              Doucette-Stamm,L., Hill,D.E. and Vidal,M.

TITLE        C. elegans ORFeome version 1.1: experimental verification of the
              genome annotation and resource for proteome-scale protein
              expression
JOURNAL      Nat. Genet. (2003) In press
COMMENT      Contact: Vidal M
              Marc Vidal Laboratory
              Dana Farber Cancer Institute
              1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
              Tel: 617 632 5180
              Fax: 617 632 5739
              Email: Marc.Vidal@dfci.harvard.edu
              Sequence tag of Gateway entry clones. The primers used were
              designed on the predicted protein encoding ORF. C. elegans ORFeome
              cloning project : Contact david_hill@dfci.harvard.edu or
              marc_vidal@dfci.harvard.edu
              POLYA=No.

FEATURES     Location/Qualifiers
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                           /note="The AD-wrmcDNA library was generated with poly(A)+
                           RNA isolated from both hermaphrodite and male N2 worms of
                           all larval stages, embryos, adults and dauers and the
                           subsequent generation of cDNAs by poly(A) priming. The
                           cDNAs were cloned into pPC86"

ORIGIN
Query Match      80.8%; Score 20.2; DB 6; Length 83;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASAKGD 25
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Db 51 AGCGTGCTTTTGTGACAACTGT 27

RESULT 5
CB400948      84 bp  mRNA  linear  EST 15-MAY-2003
LOCUS        OSTF185C6_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
DEFINITION   CB400948
ACCESSION    CB400948
VERSION      CB400948.1  GI:30742675
KEYWORDS     EST.
SOURCE       Caenorhabditis elegans
ORGANISM     Caenorhabditis elegans
REFERENCE    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
AUTHORS      1 (bases 1 to 84)
              Rebol,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M.,
              Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T.,
              Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
              Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V.,
              Tolias,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
              Doucette-Stamm,L., Hill,D.E. and Vidal,M.

TITLE        C. elegans ORFeome version 1.1: experimental verification of the
              genome annotation and resource for proteome-scale protein
              expression
JOURNAL      Nat. Genet. (2003) In press
COMMENT      Contact: Vidal M
              Marc Vidal Laboratory
              Dana Farber Cancer Institute
              1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
              Tel: 617 632 5180
              Fax: 617 632 5739
              Email: Marc.Vidal@dfci.harvard.edu
              Sequence tag of Gateway entry clones. The primers used were
              designed on the predicted protein encoding ORF. C. elegans ORFeome
              cloning project : Contact david_hill@dfci.harvard.edu or
              marc_vidal@dfci.harvard.edu
              POLYA=No.

FEATURES     Location/Qualifiers
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                           /clone_lib="AD-wrmcDNA"
                           /note="The AD-wrmcDNA library was generated with poly(A)+
                           RNA isolated from both hermaphrodite and male N2 worms of
                           all larval stages, embryos, adults and dauers and the
                           subsequent generation of cDNAs by poly(A) priming. The
                           cDNAs were cloned into pPC86"

ORIGIN
Query Match      80.8%; Score 20.2; DB 6; Length 83;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASAKGD 25
   ::::::::::::::::::::::::::::::
Db 51 AGCGTGCTTTTGTGACAACTGT 27

RESULT 5
CB400948      84 bp  mRNA  linear  EST 15-MAY-2003
LOCUS        OSTF185C6_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
DEFINITION   CB400948
ACCESSION    CB400948
VERSION      CB400948.1  GI:30742675
KEYWORDS     EST.
SOURCE       Caenorhabditis elegans
ORGANISM     Caenorhabditis elegans
REFERENCE    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
AUTHORS      1 (bases 1 to 84)
              Rebol,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M.,
              Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T.,
              Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
              Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V.,
              Tolias,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
              Doucette-Stamm,L., Hill,D.E. and Vidal,M.

TITLE        C. elegans ORFeome version 1.1: experimental verification of the
              genome annotation and resource for proteome-scale protein
              expression
JOURNAL      Nat. Genet. (2003) In press
COMMENT      Contact: Vidal M
              Marc Vidal Laboratory
              Dana Farber Cancer Institute
              1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
              Tel: 617 632 5180
              Fax: 617 632 5739
              Email: Marc.Vidal@dfci.harvard.edu
              Sequence tag of Gateway entry clones. The primers used were
              designed on the predicted protein encoding ORF. C. elegans ORFeome
              cloning project : Contact david_hill@dfci.harvard.edu or
              marc_vidal@dfci.harvard.edu
              POLYA=No.

FEATURES     Location/Qualifiers
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                           /organism="Caenorhabditis elegans"
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                           /tissue_type="whole animal"
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                           RNA isolated from both hermaphrodite and male N2 worms of
                           all larval stages, embryos, adults and dauers and the
                           subsequent generation of cDNAs by poly(A) priming. The
                           cDNAs were cloned into pPC86"

ORIGIN
Query Match      80.8%; Score 20.2; DB 6; Length 84;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASAKGD 25
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Db 35 ACCAGCGCTTTCTTGTACAAAGTGG 59

RESULT 6
CB400039/c     87 bp  mRNA  linear  EST 15-MAY-2003
LOCUS        OSTF167D8_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
DEFINITION   CB400039
ACCESSION    CB400039
VERSION      CB400039.1  GI:30741766
KEYWORDS     EST.
SOURCE       Caenorhabditis elegans
ORGANISM     Caenorhabditis elegans
REFERENCE    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
AUTHORS      1 (bases 1 to 87)
              Rebol,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M.,
              Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T.,
              Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
              Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V.,
              Tolias,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
              Doucette-Stamm,L., Hill,D.E. and Vidal,M.

TITLE        C. elegans ORFeome version 1.1: experimental verification of the
              genome annotation and resource for proteome-scale protein
              expression
JOURNAL      Nat. Genet. (2003) In press
COMMENT      Contact: Vidal M
              Marc Vidal Laboratory
              Dana Farber Cancer Institute
              1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
              Tel: 617 632 5180
              Fax: 617 632 5739
              Email: Marc.Vidal@dfci.harvard.edu
              Sequence tag of Gateway entry clones. The primers used were
              designed on the predicted protein encoding ORF. C. elegans ORFeome
              cloning project : Contact david_hill@dfci.harvard.edu or
              marc_vidal@dfci.harvard.edu
              POLYA=No.

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cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
POLYA=No.

FEATURES	SOURCE
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Location/Qualifiers

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/clone_lib="AD-wrmcDNA"
/notes="The AD-wrmcDNA library was
RNA isolated from both hermaphrodites
all larval stages, embryos, adults
subsequent generation of cDNAs by
cDNAs were cloned into pPC86"
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ORIGIN

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Query Match      80.8%; Score 20.2; DB 6; Length 87;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25
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Db 30 ACCCAGCTTTCCTGTACAAGTTGG 6

RESULT 7
CF652842

CF52842 87 bp mRNA linear EST 06-NOV-2003
80-L020166-066-001-P19-SP6P MP1Z-ADIS-066 Arabidopsis thaliana cDNA
clone MP1Zp2001P191Q 5-PRIME, mRNA sequence.

ACCESSION

CF652842.1 GI:37429718

KEYWORDS

SOURCE *Arabidopsis thaliana* (thale cress)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS Schmid, K.J., Soerensen, T.R., Stracke, R., Torjek, O., Altmann, T., Mitchell-Olds, T. and Weishaar, B.

TITLE Large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in *Arabidopsis thaliana*

JOURNAL Genome Res. 13 (6), 1250-1257 (2003)

**BOOKS
MEDLINE**

12799357
Contact: Weishaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaa@mpiz-koeln.mpg.de
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FEATURES

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/note="Vector: PCMVSPOR16; Site:
cDNA library from Arabidopsis thaliana
Wassilewskija-0; roots from three

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on MS-plates at 26W-0C with 16 hours light/day; library was made at the Max-Planck-Institute for Plant Breeding Research, Cologne, Germany; cloning sites Sali-NotI, primer sites and orientation.

SP6-Sali-CACGCGTCG-sprime-cDNA-polyA-CC-NotI-T7, GATEWAY, GABI Arabidopsis Verbund I; Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection', PI: Bernd Weisshaar Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de> This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further information."

ORIGIN

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Query Match      80.8%; Score 20.2; DB 7; Length 87;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;
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Qy

1 RBYCWGCTTTTTRTACWAASTKGD 25
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pB

44 ACCCAGCTTTCCTGTACAAAGTGTT 68

RESULT 8

CF561862
LOCUS
DEFINITION
CF561862 89 bp mRNA linear EST 06-NOV-2003
19-LJ02024-066-003-E06-SP6P MPZ-ADIS-066 Arabidopsis thaliana cdna
clone MPZp2001E063Q 5-PRIME, mRNA sequence.

ACCESSION

VERSION CF651862.1 GI:37427808

KEYWORDS

SOURCE Arabidopsis thaliana (thale cress)

ORGANIS

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 89)

AUTHORS

TITLE Large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in *Arabidopsis thaliana*

JOURNAL Genome Res. 13 (6), 1250-1257 (2003)

MEDLINE

12789357	Contact: Weisshaar B
	ADIS DNA core facility at MPIZ
	Max-Planck-Institute for Plant
	Cell-von-Linne Weg 10, 50829 Koeln, Germany
	Fax: 00492215062851
	Email: weisshaar@mpiz-koeln.mpg.de
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FEATURES

source

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 Wassilewskija-0; roots from three weeks old plants grown
 on MS-plates at 26-M°C with 16 hours light/day; library
 was made at the Max-Planck-Institute for Plant Breeding
 Research, Cologne, Germany; cloning sites Sali-NotI,
 primer sites and orientation:
 SP6-Sali-CCACGGCTCGG-3prime-cDNA-polyA-CC-NotI-7; GATEWAY

compatible; Note: Sequencing granted in the context of the GABI Arabidopsis Verbund I: Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection' PI: Bernd Weisshaar Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de> This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further information."

ORIGIN

Query Match 80.8%; Score 20.2; DB 7; Length 89;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25
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Db 44 ACCCAGCTTCTTGTACAAAGTGCT 68

RESULT 9
CF652759
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CF652759
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM Arabidopsis thaliana (thale cress)

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MP12
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
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Seq primer: SP6P;..

FEATURES

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/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from Arabidopsis thaliana, accession Wassilewskija-0; roots from three weeks old plants grown on MS-plates at 26M-OC with 16 hours light/day; library was made at the Max-Planck-Institute for Plant Breeding Research, Cologne, Germany; Cloning sites SalI-NotI, primer sites and orientation:
SP6-Sali-CCACGCGCCG-5prime-cDNA-polyA-CC-NotI-T7; GATEWAY compatible; Note: Sequencing granted in the context of the GABI Arabidopsis Verbund I: Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection' PI: Bernd Weisshaar Sequence submission managed

by RZPD/GABI-Primary database: <http://gabi.rzpd.de> This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further information."

ORIGIN

Query Match 80.8%; Score 20.2; DB 7; Length 89;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25
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Db 44 ACCCAGCTTCTTGTACAAAGTGCT 68

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CF653076
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM Arabidopsis thaliana (thale cress)

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MP12
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
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FEATURES

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/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from Arabidopsis thaliana, accession Wassilewskija-0; roots from three weeks old plants grown on MS-plates at 26M-OC with 16 hours light/day; library was made at the Max-Planck-Institute for Plant Breeding Research, Cologne, Germany; Cloning sites SalI-NotI, primer sites and orientation:
SP6-Sali-CCACGCGCCG-5prime-cDNA-polyA-CC-NotI-T7; GATEWAY compatible; Note: Sequencing granted in the context of the GABI Arabidopsis Verbund I: Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection' PI: Bernd Weisshaar Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de> This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further information."

ORIGIN

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Query Match      80.8%; Score 20.2; DB 7; Length 89;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25
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Db 44 ACCCAGCTTCTTGACAAAGTGGT 68

RESULT 11
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LOCUS      90 bp      mRNA      linear      EST 15-MAY-2003
DEFINITION OSTF163A10_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION  CB392047
VERSION     CB392047.1 GI:30733757
KEYWORDS   EST.
SOURCE     Caenorhabditis elegans
ORGANISM   Caenorhabditis elegans
REFERENCE  1 (bases 1 to 90)
AUTHORS    Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M.,
            Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T.,
            Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
            Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V.,
            Tollas, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
            Doucette-Stamm, L., Hill, D.E. and Vidal, M.
TITLE      C. elegans ORFeome version 1.1: experimental verification of the
            genome annotation and resource for proteome-scale protein
            expression
JOURNAL    Nat. Genet. (2003) In press
COMMENT    Contact: Vidal M
            Dana Farber Cancer Institute
            1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
            Tel: 617 632 5180
            Fax: 617 632 5739
            Email: Marc.Vidal@dfci.harvard.edu
            Sequence tag of Gateway entry clones. The primers used were
            designed on the predicted protein encoding ORF. C. elegans ORFeome
            cloning project : Contact david_hill@dfci.harvard.edu or
            marc_vidal@dfci.harvard.edu
POLYA=No.

FEATURES             Location/Qualifiers
     source            1..90
     -
     /organism="Caenorhabditis elegans"
     /mol_type="mRNA"
     /strain="N2"
     /db_xref="taxon:6239"
     /sex="Hermaphrodite and male"
     /tissue_type="whole animal"
     /dev_stage="mixed stage"
     /clone_lib="AD-wrmcDNA"
     /note="The AD-wrmcDNA library was generated with poly(A)+
            RNA isolated from both hermaphrodite and male N2 worms of
            all larval stages, embryos, adults and dauers and the
            subsequent generation of cDNAs by poly(A) priming. The
            cDNAs were cloned into pPC86"

ORIGIN
Query Match      80.8%; Score 20.2; DB 6; Length 90;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RBYCWGCTTTTTRTACWAASTKGD 25
   :::::::::::::::::::::
Db 35 ACCCAGCTTCTTGACAAAGTGG 11

RESULT 13
CB652843
LOCUS      93 bp      mRNA      linear      EST 06-NOV-2003
DEFINITION CB10-L020167-066-001-P20-SP6P MP1Z-ADIS-066 Arabidopsis thaliana cDNA
            clone MP1Zp2001P20IQ 5-PRIME, mRNA sequence.
ACCESSION  CF652843
VERSION     CF652843.1 GI:37429720
KEYWORDS   EST.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
REFERENCE  1 (bases 1 to 93)
AUTHORS    Schmid, K.J., Soerensen, T.R., Stracke, R., Torjek, O., Altmann, T.,
            Mitchell-Olds, T. and Weishaar, B.
TITLE      Large-scale identification and analysis of genome-wide

```



```

1. 95
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmCDNA"
/note="The AD-wrmCDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pC86"

```

ORIGIN

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Query Match      80.8%; Score 20.2; DB 6; Length 95;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 15; Conservative 10; Mismatches 0; Indels 0; Caps 0;
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:::|::|::|::|::|::|::|:
Db 32 ACCCAGCTTTCCTGTACAAGTTGG 8

Search completed: November 16, 2004, 10:16:34
Job time : 1532 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	21.8	87.2	25	6	AR124526	Sequence
2	21.8	87.2	25	6	AR124527	Sequence
3	21.8	87.2	25	6	AR124528	Sequence
4	21.8	87.2	25	6	AR124551	Sequence
C 5	21.8	87.2	25	6	AR124552	Sequence
C 6	21.8	87.2	25	6	AR124553	Sequence
C 7	21.8	87.2	25	6	AR124554	Sequence
C 8	21.8	87.2	25	6	AR124555	Sequence
9	21.8	87.2	25	6	AR163177	Sequence
10	21.8	87.2	25	6	AR163178	Sequence
11	21.8	87.2	25	6	AR163179	Sequence
12	21.8	87.2	25	6	AR163202	Sequence
C 13	21.8	87.2	25	6	AR163203	Sequence
C 14	21.8	87.2	25	6	AR163204	Sequence
C 15	21.8	87.2	25	6	AR163205	Sequence
C 16	21.8	87.2	25	6	AR163206	Sequence
C 17	21.8	87.2	25	6	BD263223	Compositi
C 18	21.8	87.2	25	6	BD263224	Compositi
C 19	21.8	87.2	25	6	BD263313	Compositi

[illegible]

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:29:13 ; Search time 167.8 Seconds
(without alignments)
782.095 Million cells updates/sec

Title: US-10-820-133-40
Perfect score: 25
Sequence: 1 ascwgttctttracwaaatkqw 25

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001as.*
5: Geneseq2001bs.*
6: Geneseq2002as.*
7: Geneseq2002bs.*
8: Geneseq2003as.*
9: Geneseq2003bs.*
10: Geneseq2003cs.*
11: Geneseq2003ds.*
12: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21.8	87.2	25	2	AAT48216
2	21.8	87.2	25	2	AAT48215
3	21.8	87.2	25	2	AAT48217
4	21.8	87.2	25	2	AAX78994
5	21.8	87.2	25	2	AAX78940
6	21.8	87.2	25	2	AAX78942
7	21.8	87.2	25	2	AAX78941
8	21.8	87.2	25	2	AAX78974
9	21.8	87.2	25	3	AAC55381
10	21.8	87.2	25	3	AAC55380
11	21.8	87.2	25	3	AAC55380
12	21.8	87.2	25	4	AAS06178
13	21.8	87.2	25	4	AAS06182
14	21.8	87.2	25	4	AAS06276
15	21.8	87.2	25	4	AAC87873
16	21.8	87.2	25	4	AAC87899
17	21.8	87.2	25	4	AAC87897
18	21.8	87.2	25	4	AAC87898
19	21.8	87.2	25	4	AAC87872
20	21.8	87.2	25	4	AAC87871
21	21.8	87.2	25	4	AAC87896

ALIGNMENTS

RESULT 1

AAT48216

ID AAT48216 standard; DNA; 25 BP.

XX AC AAT48216;

DT 20-OCT-1997 (first entry)

XX DB attB2 core region.

XX att recombination site; core region; mutation; enhance; recombination;

XX vector; subcloning; regulation; exchange; ss.

XX Synthetic.

XX WO9640724-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US010082.

XX 07-JUN-1995; 95US-00486139.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA;

XX WPI, 1997-065168/06.

XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid - using recombinant proteins and engineered recombination sites in vitro or in vivo.

XX Claim 14; Page 55; 106pp; English.

XX AAT48210-25 are att recombination site core region DNA sequences. The core region has at least one engineered mutation that enhances recombination in vitro in the formation of a Cointegrate or Product DNA. These core regions can be incorporated into novel vector donor DNA molecules. The nucleic acids, vectors and methods of the invention are used to obtain chimeric nucleic acid using recombination proteins and engineered recombination sites in vitro or in vivo. The improved specificity, speed and yields of the invention facilitates DNA or RNA subcloning, regulation or exchange useful for any related purpose, e.g.

Aac87900 Escherich
Aaf55740 Recombina
Aaf55767 PCR prime
Aaf55765 Recombina
Aaf55742 Recombina
Aaf55768 PCR prime
Aaf55741 Recombina
Aaf55766 PCR prime
Aaf55769 PCR prime
Aah22543 ATT site
Aah22542 ATT site
Aad14434 Recombina
Aad14459 Recombina
Aad14435 Recombina
Aad14435 Recombina
Abq82120 Core sequ
Abq82118 Core sequ
Abq82119 Core sequ
Abt16626 Artificia
Abt16627 Artificia
Acd28428 Engineere
Acd28281 Nucleic a
Acd28282 Nucleic a
Acd28426 Wild type

CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
CC or modification of transcribed, replicated, isolated or genomic DNA or
CC RNA

XX SQ Sequence 25 BP; 5 A; 6 C; 4 G; 10 T; 0 U; 0 Other;

Query Match 87.2%; Score 21.8; DB 2; Length 25;

Best Local Similarity 68.0%; Pred. No. 5.4;

Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASCCGCTTTTCTTACAACTGT 25

Db 1 AGCCTGCTTTCTTGTACAACTGT 25

RESULT 2

AAT48215

ID AAT48215 standard; DNA; 25 BP.

XX AC AAT48215;

XX AC AAT48215;

DT 20-OCT-1997 (first entry)

DE attB1 core region.

XX att recombination site; core region; mutation; enhance; recombination;

KW vector; subcloning; regulation; exchange; ss.

XX Synthetic.

XX WO9640724-A1.

XX PD 19-DEC-1996.

XX PF 07-JUN-1996; 96WO-US010082.

XX PR 07-JUN-1995; 95US-00486139.

XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Hartley JL, Brasch MA;

XX WPI; 1997-065168/06.

XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -

PT using recombinant proteins and engineered recombination sites in vitro or

PT in vivo.

PS Claim 14; Page 55; 106pp; English.

XX AAT48210-25 are att recombination site core region DNA sequences. The

CC core region has at least one engineered mutation that enhances

CC recombination in vitro in the formation of a Cointegrate or Product DNA.

CC These core regions can be incorporated into novel vector donor DNA

CC molecules. The nucleic acids, vectors and methods of the invention are

CC used to obtain chimeric nucleic acid using recombination proteins and

CC engineered recombination sites in vitro or in vivo. The improved

CC specificity, speed and yields of the invention facilitates DNA or RNA

CC subcloning, regulation or exchange useful for any related purpose, e.g.

CC in vitro recombination of DNA segments, and in vitro or in vivo insertion

CC or modification of transcribed, replicated, isolated or genomic DNA or

CC RNA

XX SQ Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 U; 0 Other;

Query Match 87.2%; Score 21.8; DB 2; Length 25;

Best Local Similarity 68.0%; Pred. No. 5.4;

Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASCCGCTTTTCTTACAACTGT 25

Db 1 AGCCTGCTTTTGTACAACTGT 25

RESULT 3

AAT48217

ID AAT48217 standard; DNA; 25 BP.

XX AC AAT48217;

XX AC AAT48217;

DT 20-OCT-1997 (first entry)

DE attB3 core region.

XX att recombination site; core region; mutation; enhance; recombination;

KW vector; subcloning; regulation; exchange; ss.

XX Synthetic.

XX WO9640724-A1.

XX PD 19-DEC-1996.

XX PF 07-JUN-1996; 96WO-US010082.

XX PR 07-JUN-1995; 95US-00486139.

XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Hartley JL, Brasch MA;

XX WPI; 1997-065168/06.

XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -

PT using recombinant proteins and engineered recombination sites in vitro or

PT in vivo.

XX Claim 14; Page 55; 106pp; English.

XX AAT48210-25 are att recombination site core region DNA sequences. The

CC core region has at least one engineered mutation that enhances

CC recombination in vitro in the formation of a Cointegrate or Product DNA.

CC These core regions can be incorporated into novel vector donor DNA

CC molecules. The nucleic acids, vectors and methods of the invention are

CC used to obtain chimeric nucleic acid using recombination proteins and

CC engineered recombination sites in vitro or in vivo. The improved

CC specificity, speed and yields of the invention facilitates DNA or RNA

CC subcloning, regulation or exchange useful for any related purpose, e.g.

CC in vitro recombination of DNA segments, and in vitro or in vivo insertion

CC or modification of transcribed, replicated, isolated or genomic DNA or

CC RNA

XX SQ Sequence 25 BP; 6 A; 7 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 87.2%; Score 21.8; DB 2; Length 25;

Best Local Similarity 68.0%; Pred. No. 5.4;

Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASCCGCTTTTCTTACAACTGT 25

Db 1 ACCCAGCTTTCTTGTACAACTGT 25

RESULT 4

AAAX78994

ID AAAX78994 standard; DNA; 25 BP.

XX AC AAAX78994;

XX AC AAAX78994;

DT 17-AUG-1999 (first entry)

DE Oligonucleotide #60 for recombination and cloning method.

XX Cloning; donor; recombination site; vector; chimeric; ss.

XX Synthetic.

```
XX WO9921977-A1.
XX 06-MAY-1999.
XX 26-OCT-1998; 98WO-US022589.
XX 24-OCT-1997; 97US-0065930P.
XX 23-OCT-1998; 98US-00177387.
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX Hartley JL, Brasch MA, Temple GF, Fox DK;
XX WPI; 1999-303011/25.
XX New nucleic acid cloning methods.
XX Disclosure; Page 176; 185pp; English.
XX The invention relates to novel methods for cloning or subcloning one or
XX more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
XX in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
XX more desired nucleic acid segments flanked by at least 2 recombination
XX sites which do not recombine with each other; (2) one or more vector
XX donor molecules (VDMs) comprising at least 2 recombination sites which do
XX not recombine with each other; and (3) one or more site-specific
XX recombination proteins; (b) incubating the combination to transfer one or
XX more of the desired segments into one or more of the VDMs, thereby
XX producing one or more desired product molecules (PMs). The methods can be
XX used for the efficient and specific recombination of NAM segments. They
XX can be used to generate chimeric DNA or RNA molecules that have the
XX desired characteristics and/or nucleic acid segments. The methods can
XX also be used for changing vectors. The oligonucleotides AAX78935-X78994
XX are used in the method of the invention
XX Sequence 25 BP; 6 A; 5 C; 3 G; 11 T; 0 U; 0 Other;
XX Query Match 87.2%; Score 21.8; DB 2; Length 25;
XX Best Local Similarity 68.0%; Pred. No. 5.4;
XX Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ASCCGCTTTTATTACWAASTKGW 25
Db 1 AGCCTGCTTTTATTACTAAGTTGA 25
RESULT 5
AAX78940
ID AAX78940 standard; DNA; 25 BP.
XX AC
XX AAX78940;
XX 17-AUG-1999 (first entry)
XX Oligonucleotide #6 for recombination and cloning method.
XX Cloning; donor; recombination site; vector; chimeric; ss.
XX Synthetic.
XX WO9921977-A1.
XX 06-MAY-1999.
XX 26-OCT-1998; 98WO-US022589.
XX 24-OCT-1997; 97US-0065930P.
XX 23-OCT-1998; 98US-00177387.
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX Hartley JL, Brasch MA, Temple GF, Fox DK;
XX WPI; 1999-303011/25.
XX New nucleic acid cloning methods.
XX Disclosure; Page 176; 185pp; English.
XX The invention relates to novel methods for cloning or subcloning one or
XX more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
XX in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
XX more desired nucleic acid segments flanked by at least 2 recombination
XX sites which do not recombine with each other; (2) one or more vector
XX donor molecules (VDMs) comprising at least 2 recombination sites which do
XX not recombine with each other; and (3) one or more site-specific
XX recombination proteins; (b) incubating the combination to transfer one or
XX more of the desired segments into one or more of the VDMs, thereby
XX producing one or more desired product molecules (PMs). The methods can be
XX used for the efficient and specific recombination of NAM segments. They
XX can be used to generate chimeric DNA or RNA molecules that have the
XX desired characteristics and/or nucleic acid segments. The methods can
XX also be used for changing vectors. The oligonucleotides AAX78935-X78994
XX are used in the method of the invention
XX Sequence 25 BP; 6 A; 5 C; 3 G; 11 T; 0 U; 0 Other;
XX Query Match 87.2%; Score 21.8; DB 2; Length 25;
XX Best Local Similarity 68.0%; Pred. No. 5.4;
XX Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ASCCGCTTTTATTACWAASTKGW 25
Db 1 AGCCTGCTTTTATTACTAAGTTGA 25
RESULT 6
AAX78942
ID AAX78942 standard; DNA; 25 BP.
XX AC
XX AAX78942;
XX 17-AUG-1999 (first entry)
XX Oligonucleotide #8 for recombination and cloning method.
XX Cloning; donor; recombination site; vector; chimeric; ss.
XX Synthetic.
XX WO9921977-A1.
XX 06-MAY-1999.
XX 26-OCT-1998; 98WO-US022589.
XX 24-OCT-1997; 97US-0065930P.
XX 23-OCT-1998; 98US-00177387.
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX Hartley JL, Brasch MA, Temple GF, Fox DK;
XX WPI; 1999-303011/25.
XX New nucleic acid cloning methods.
XX Disclosure; Page 160; 185pp; English.
XX The invention relates to novel methods for cloning or subcloning one or
XX more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
XX in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
XX more desired nucleic acid segments flanked by at least 2 recombination
XX sites which do not recombine with each other; (2) one or more vector
XX donor molecules (VDMs) comprising at least 2 recombination sites which do
XX not recombine with each other; and (3) one or more site-specific
XX recombination proteins; (b) incubating the combination to transfer one or
XX more of the desired segments into one or more of the VDMs, thereby
XX producing one or more desired product molecules (PMs). The methods can be
XX used for the efficient and specific recombination of NAM segments. They
XX can be used to generate chimeric DNA or RNA molecules that have the
XX desired characteristics and/or nucleic acid segments. The methods can
XX also be used for changing vectors. The oligonucleotides AAX78935-X78994
XX are used in the method of the invention
XX Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 U; 0 Other;
XX Query Match 87.2%; Score 21.8; DB 2; Length 25;
XX Best Local Similarity 68.0%; Pred. No. 5.4;
XX Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ASCCGCTTTTATTACWAASTKGW 25
Db 1 AGCCTGCTTTTATTACTAAGTTGT 25
RESULT 6
AAX78942
ID AAX78942 standard; DNA; 25 BP.
XX AC
XX AAX78942;
XX 17-AUG-1999 (first entry)
XX Oligonucleotide #8 for recombination and cloning method.
XX Cloning; donor; recombination site; vector; chimeric; ss.
XX Synthetic.
XX WO9921977-A1.
XX 06-MAY-1999.
XX 26-OCT-1998; 98WO-US022589.
XX 24-OCT-1997; 97US-0065930P.
XX 23-OCT-1998; 98US-00177387.
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX Hartley JL, Brasch MA, Temple GF, Fox DK;
XX WPI; 1999-303011/25.
XX New nucleic acid cloning methods.
XX Disclosure; Page 160; 185pp; English.
XX The invention relates to novel methods for cloning or subcloning one or
XX more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
XX in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
XX more desired nucleic acid segments flanked by at least 2 recombination
XX sites which do not recombine with each other; (2) one or more vector
XX donor molecules (VDMs) comprising at least 2 recombination sites which do
XX not recombine with each other; and (3) one or more site-specific
XX recombination proteins; (b) incubating the combination to transfer one or
XX more of the desired segments into one or more of the VDMs, thereby
XX producing one or more desired product molecules (PMs). The methods can be
XX used for the efficient and specific recombination of NAM segments. They
XX can be used to generate chimeric DNA or RNA molecules that have the
XX desired characteristics and/or nucleic acid segments. The methods can
XX also be used for changing vectors. The oligonucleotides AAX78935-X78994
XX are used in the method of the invention
XX Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 U; 0 Other;
```



```

XX 11-JAN-2001 (first entry)
DT Recombination site nucleotide sequence attB2.
DE
XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX Bacteriophage lambda.
OS
XX WO200052027-A1.
PN
XX 08-SEP-2000.
PD
XX 02-MAR-2000; 2000WO-US005432.
PF
XX 02-MAR-1999; 99US-0122389P.
PR
XX 23-MAR-1999; 99US-0126049P.
PR
XX 28-MAY-1999; 99US-0136744P.
PR
XX (LIFE-) LIFE TECHNOLOGIES INC.
PA
XX Hartley JL, Brasch MA, Temple GF, Cheo D;
PI WPI; 2000-543948/49.
XX
DR Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
XX attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
XX recombinational cloning of polypeptides.
XX Claim 1; Fig 9; 459pp; English.
XX
XX The present invention describes isolated nucleic acid molecules (I)
XX encoding an attB1, attB2, attP1, attL1, attL2, attR1, and attR2
XX nucleotide sequence. Also described are: (1) an isolated nucleic acid
XX molecule (II) comprising one or more att recombination sites comprising
XX at least one mutation in its core region that increases the specificity
XX of interaction between the recombination site and a second att
XX recombination site; and (2) an isolated nucleic acid molecule (III)
XX comprising one or more mutated att recombination sites comprising at
XX least one mutation in its core region that enhances the efficiency of
XX recombination between a first nucleic acid molecule comprising the
XX mutated att recombination site and a second nucleic acid molecule
XX comprising a second recombination site that interacts with the mutated
XX att recombination site. (I), (II), (III), primers, vectors and methods
XX from the present invention are used for the recombinational cloning of
XX nucleic acid molecules. They can be used for changing vectors, targeting
XX gene products to intracellular locations, cleaving fusion tags from
XX desired proteins, operably linking nucleic acid molecules of interest to
XX regulatory genetic sequences, constructing genes for fusion proteins,
XX changing copy number, changing replicons, cloning into phages and
XX cloning. (I), (II), (III), host cells and vectors can be used in the
XX production of polypeptides and antibodies. The present sequence is used
XX in the exemplification of the present invention
XX
SQ Sequence 25 BP; 6 A; 6 C; 5 G; 8 T; 0 U; 0 Other;
Query Match 87.2%; Score 21.8; DB 3; Length 25;
Best Local Similarity 68.0%; Pred. No. 5.4;
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
Oy 1 ASCCGCTTTTCTGTACAAAGTGGT 25
Db 1 ACCGAGCTTTCTGTACAAAGTGGT 25
RESULT 10
AAC55380/c
ID AAC55380 standard; DNA; 25 BP.
XX
XX AAC55380;
AC
XX

```

```
XX DE Recombination efficiency with mutated attB2 site oligonucleotide attB0.
XX DE Bacteriophage lambda; att; recombination site; attB; attP; attB; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; PCR primer; ss.
XX OS Bacteriophage lambda.
OS Synthetic.
FN WO200052027-A1.
XX .
XX PD 08-SEP-2000.
XX PD 02-MAR-2000; 2000WO-US005432.
XX PF 02-MAR-1999; 99US-0122389P.
XX PR 23-MAR-1999; 99US-0126049P.
XX PR 28-MAY-1999; 99US-0136744P.
XX XX (LIFE-) LIFE TECHNOLOGIES INC.
XX XX
XX PI Hartley JL, Brasch MA, Temple GF, Cheo D;
XX WPI; 2000-543948/49.
XX DR
XX XX
XX PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
XX attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
XX recombinational cloning of polypeptides.
XX PT
XX PS Example 23; Page 157; 459pp; English.
XX PS
XX CC The present invention describes isolated nucleic acid molecules (I)
XX CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
XX CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
XX CC molecule (II) comprising one or more att recombination sites comprising
XX CC at least one mutation in its core region that increases the specificity
XX CC of interaction between the recombination site and a second att
XX CC recombination site; and (2) an isolated nucleic acid molecule (III)
XX CC comprising one or more mutated att recombination sites comprising at
XX CC least one mutation in its core region that enhances the efficiency of
XX CC recombination between a first nucleic acid molecule comprising the
XX CC mutated att recombination site and a second nucleic acid molecule
XX CC comprising a second recombination site that interacts with the mutated
XX CC att recombination site. (I), (II), (III), primers, vectors and methods
XX CC from the present invention are used for the recombinational cloning of
XX CC nucleic acid molecules. They can be used for changing vectors, targeting
XX CC gene products to intracellular locations, cleaving fusion tags from
XX CC desired proteins, operably linking nucleic acid molecules of interest to
XX CC regulatory genetic sequences, constructing genes for fusion proteins,
XX CC changing copy number, changing replicons, cloning into phages and
XX CC cloning (I), (II), (III), host cells and vectors can be used in the
XX CC production of polypeptides and antibodies. The present sequence is used
XX CC in the exemplification of the present invention
XX SQ Sequence 25 BP; 11 A; 3 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 87.2%; Score 21.8; DB 3; Length 25;
Best Local Similarity 68.0%; Pred. No. 5.4;
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASCCGCTTTTTRTACAAATKGW 25
DB 25 AGCCTGCTTTTATTACTACTTGA 1

RESULT 12
AAS06178
ID AAS06178 standard; DNA; 25 BP.
XX AC AAS06178;
XX DT 12-SEP-2001 (first entry)

Query Match 87.2%; Score 21.8; DB 3; Length 25;
Best Local Similarity 68.0%; Pred. No. 5.4;
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASCCGCTTTTTRTACAAATKGW 25
DB 25 AGCCTGCTTTTATTACTACTTGA 1

RESULT 13
AAS06182
ID AAS06182 standard; DNA; 25 BP.
XX AC AAS06182;
XX DT 12-SEP-2001 (first entry)
Phage-lambda recombination site attB2.
XX DE Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
KW lambda integrase; therapeutic; ss.
XX KW lambda integrase; therapeutic; ss.
XX OS Bacteriophage lambda.
XX WO200142509-A1.
XX PN 14-JUN-2001.
XX PD 11-DEC-2000; 2000WO-US033546.
XX PF 10-DEC-1999; 99US-0169983P.
XX PR 09-MAR-2000; 2000US-0188020P.
XX XX (CHEO/) CHEO D.
XX PA (BRAS/) BRASCH M A.
XX PA (TEMP/) TEMPLE G F.
XX PA (HART/) HARTLEY J L.
XX PA (BYRD/) BYRD D R N.
XX XX Cheo D, Brasch MA, Temple GF, Hartley JL, Byrd DRN;
XX WPI; 2001-356174/37.
XX DR
XX XX
XX PT Producing hybrid nucleic acids, useful for expressing novel therapeutic
XX PT polypeptides, by mixing the same or different nucleic acids having one or
XX FT more recombination sites in the presence of recombination proteins, e.g.
XX FT Cre.
XX PT
XX PS Disclosure; Fig 24A; 357pp; English.
XX PS
XX CC AAS06174-AAS06322 represent Bacteriophage lambda att recombination site
XX CC nucleic acid sequences, and PCR primers of the invention. The att
XX CC sequences are recognised by the recombination protein lambda integrase
XX CC (Int). The invention is a new method of producing a population of hybrid
XX CC nucleic acids comprising mixing at least a first population of nucleic
XX CC acids comprising one or more recombination sites with at least one target
XX CC nucleic acid comprising one or more recombination sites and causing some
XX CC or all of the nucleic acids to recombine with all or some of the target
XX CC nucleic acids. The method is useful for producing a population of hybrid
XX CC nucleic acids which may be the same or different. The nucleic acids may
XX CC be used to express therapeutic proteins or peptides and they may also be
XX CC used to create novel fusion proteins by expressing different sequences
XX CC linked to each other. The method allows simultaneous cloning of two or
XX CC more different nucleic acids
XX SQ Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 U; 0 Other;

Query Match 87.2%; Score 21.8; DB 4; Length 25;
Best Local Similarity 68.0%; Pred. No. 5.4;
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASCCGCTTTTTRTACAAATKGW 25
DB 1 AGCCTGCTTTTATTACTACTTGT 25

RESULT 13
AAS06182
ID AAS06182 standard; DNA; 25 BP.
XX AC AAS06182;
XX DT 12-SEP-2001 (first entry)
Phage-lambda recombination site attB2.
XX DE Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
KW lambda integrase; therapeutic; ss.
XX KW lambda integrase; therapeutic; ss.
XX OS Bacteriophage lambda.
XX WO200142509-A1.
XX PN 14-JUN-2001.
XX PD 11-DEC-2000; 2000WO-US033546.
XX PF 10-DEC-1999; 99US-0169983P.
XX PR 09-MAR-2000; 2000US-0188020P.
XX XX (CHEO/) CHEO D.
XX PA (BRAS/) BRASCH M A.
XX PA (TEMP/) TEMPLE G F.
XX PA (HART/) HARTLEY J L.
XX PA (BYRD/) BYRD D R N.
XX XX Cheo D, Brasch MA, Temple GF, Hartley JL, Byrd DRN;
XX WPI; 2001-356174/37.
XX DR
XX XX
XX PT Producing hybrid nucleic acids, useful for expressing novel therapeutic
XX PT polypeptides, by mixing the same or different nucleic acids having one or
XX FT more recombination sites in the presence of recombination proteins, e.g.
XX FT Cre.
XX PT
XX PS Disclosure; Fig 24A; 357pp; English.
XX PS
XX CC AAS06174-AAS06322 represent Bacteriophage lambda att recombination site
XX CC nucleic acid sequences, and PCR primers of the invention. The att
XX CC sequences are recognised by the recombination protein lambda integrase
XX CC (Int). The invention is a new method of producing a population of hybrid
XX CC nucleic acids comprising mixing at least a first population of nucleic
XX CC acids comprising one or more recombination sites with at least one target
XX CC nucleic acid comprising one or more recombination sites and causing some
XX CC or all of the nucleic acids to recombine with all or some of the target
XX CC nucleic acids. The method is useful for producing a population of hybrid
XX CC nucleic acids which may be the same or different. The nucleic acids may
XX CC be used to express therapeutic proteins or peptides and they may also be
XX CC used to create novel fusion proteins by expressing different sequences
XX CC linked to each other. The method allows simultaneous cloning of two or
XX CC more different nucleic acids
XX SQ Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 U; 0 Other;
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```

OS Bacteriophage lambda.
XX WO200142509-A1.
PN
XX
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XX PD
XX
XX PF
XX 11-DEC-2000; 2000WO-US033546.
XX
XX 10-DEC-1999; 99US-0169983P.
PR
XX 09-MAR-2000; 2000US-0188020P.
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XX (CHEO/) CHEO D.
XX (BRAS/) BRASCH M A.
XX (TEMP/) TEMPLE G F.
XX (HART/) HARTLEY J L.
XX (BYRD/) BYRD D R N.
XX
XX Cheo D, Brasch MA, Temple GF, Hartley JL, Byrd DRN;
XX WPI; 2001-356174/37.
XX
XX Producing hybrid nucleic acids, useful for expressing novel therapeutic
XX polypeptides, by mixing the same or different nucleic acids having one or
XX more recombination sites in the presence of recombination proteins, e.g.
XX Cre.
XX
XX Disclosure; Fig 24A; 357pp; English.
XX
XX AAS06174-AAS06322 represent Bacteriophage lambda att recombination site
XX nucleic acid sequences, and PCR primers of the invention. The att
XX sequences are recognised by the recombination protein lambda integrase
XX (Int). The invention is a new method of producing a population of hybrid
XX nucleic acids comprising mixing at least a first population of nucleic
XX acids comprising one or more recombination sites with at least one target
XX nucleic acid comprising one or more recombination sites and causing some
XX or all of the nucleic acids to recombine with all or some of the target
XX nucleic acids. The method is useful for producing a population of hybrid
XX nucleic acids which may be the same or different. The nucleic acids may
XX be used to express therapeutic proteins or peptides and they may also be
XX used to create novel fusion proteins by expressing different sequences
XX linked to each other. The method allows simultaneous cloning of two or
XX more different nucleic acids
XX
XX SQ Sequence 25 BP; 6 A; 6 C; 5 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 87.2%; Score 21.8; DB 4; Length 25;
XX Best Local Similarity 68.0%; Pred. No. 5.4;
XX Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 ASCCGCTTTTTRTACWAATKGM 25
XX :||:||||:||||:||||:||||:
XX 1 ACCCAGCTTCTGTGACAAAGTGGT 25
XX
XX RESULT 14
XX AAS06276/C
XX ID AAS06276 standard; DNA; 25 BP.
XX
XX AC AAS06276;
XX
XX DT 12-SEP-2001 (first entry)
XX
XX DE PCR primer attB0 used to produce a population of hybrid DNA molecules.
XX
XX KW Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
XX lambda integrase; therapeutic; ss.
XX
XX OS Bacteriophage lambda.
XX OS Synthetic.
XX
XX PN WO200142509-A1.
XX
XX PD 14-JUN-2001.

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XX 11-DEC-2000; 2000WO-US033546.
XX
XX 10-DEC-1999; 99US-0169983P.
PR
XX 09-MAR-2000; 2000US-0188020P.
XX
XX (CHEO/) CHEO D.
XX (BRAS/) BRASCH M A.
XX (TEMP/) TEMPLE G F.
XX (HART/) HARTLEY J L.
XX (BYRD/) BYRD D R N.
XX
XX Cheo D, Brasch MA, Temple GF, Hartley JL, Byrd DRN;
XX WPI; 2001-356174/37.
XX
XX Producing hybrid nucleic acids, useful for expressing novel therapeutic
XX polypeptides, by mixing the same or different nucleic acids having one or
XX more recombination sites in the presence of recombination proteins, e.g.
XX Cre.
XX
XX Example 11; Page 227; 357pp; English.
XX
XX AAS06174-AAS06322 represent Bacteriophage lambda att recombination site
XX nucleic acid sequences, and PCR primers of the invention. The att
XX sequences are recognised by the recombination protein lambda integrase
XX (Int). The invention is a new method of producing a population of hybrid
XX nucleic acids comprising mixing at least a first population of nucleic
XX acids comprising one or more recombination sites with at least one target
XX nucleic acid comprising one or more recombination sites and causing some
XX or all of the nucleic acids to recombine with all or some of the target
XX nucleic acids. The method is useful for producing a population of hybrid
XX nucleic acids which may be the same or different. The nucleic acids may
XX be used to express therapeutic proteins or peptides and they may also be
XX used to create novel fusion proteins by expressing different sequences
XX linked to each other. The method allows simultaneous cloning of two or
XX more different nucleic acids
XX
XX SQ Sequence 25 BP; 11 A; 3 C; 5 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 87.2%; Score 21.8; DB 4; Length 25;
XX Best Local Similarity 68.0%; Pred. No. 5.4;
XX Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 ASCCGCTTTTTRTACWAATKGM 25
XX :||:||||:||||:||||:||||:
XX 25 AGCCTGCTTTTATATACTAATTGA 1
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XX Db
XX
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XX AAC87873
XX ID AAC87873 standard; DNA; 25 BP.
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XX AC AAC87873;
XX
XX DT 02-MAR-2001 (first entry)
XX
XX DE Escherichia coli core region recombinant site attB3 SEQ ID NO:8.
XX
XX KW Core region; recombination site; cloning; chimeric DNA; characteristic;
XX mutation; att site; lox site; ss.
XX
XX OS Escherichia coli.
XX
XX PN US6143557-A.
XX
XX PD 07-NOV-2000.
XX
XX PF 20-JAN-1999; 99US-00233493.
XX
XX PR 07-JUN-1995; 95US-00486139.
XX 07-JUN-1996; 96US-00663002.
XX 12-JAN-1998; 98US-00005476.
XX

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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:19 ; Search time 35.9 Seconds
(without alignments)
494.978 Million cell updates/sec

Title: US-10-820-133-40

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Sequence: 1 ascwgcttcttctacwaastkgw 25

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	21.8	87.2	25	3	US-09-233-493-8
4	21.8	87.2	25	3	US-09-233-493-31
5	21.8	87.2	25	3	US-09-233-493-32
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8	21.8	87.2	25	3	US-09-233-493-35
9	21.8	87.2	25	3	US-09-005-476-6
10	21.8	87.2	25	3	US-09-005-476-7
11	21.8	87.2	25	3	US-09-005-476-8
12	21.8	87.2	25	3	US-09-005-476-31
13	21.8	87.2	25	3	US-09-005-476-32
14	21.8	87.2	25	3	US-09-005-476-33
15	21.8	87.2	25	3	US-09-005-476-34
16	21.8	87.2	25	3	US-09-005-476-35
17	21.8	87.2	25	3	US-09-233-492-6
18	21.8	87.2	25	3	US-09-233-492-7
19	21.8	87.2	25	3	US-09-233-492-8
20	21.8	87.2	25	3	US-09-233-492-31
21	21.8	87.2	25	3	US-09-233-492-32
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23	21.8	87.2	25	3	US-09-233-492-34
24	21.8	87.2	25	3	US-09-233-492-35
25	21.8	87.2	25	3	US-09-296-280-6
26	21.8	87.2	25	3	US-09-296-280-7
27	21.8	87.2	25	3	US-09-296-280-8

28	21.8	87.2	25	3	US-09-296-280-40	Sequence 40, Appl
29	21.8	87.2	25	3	US-09-296-280-60	Sequence 60, Appl
30	21.8	87.2	25	4	US-09-498-074-6	Sequence 6, Appl
31	21.8	87.2	25	4	US-09-498-074-7	Sequence 7, Appl
32	21.8	87.2	25	4	US-09-498-074-8	Sequence 8, Appl
33	21.8	87.2	25	4	US-09-498-074-31	Sequence 31, Appl
34	21.8	87.2	25	4	US-09-498-074-32	Sequence 32, Appl
35	21.8	87.2	25	4	US-09-498-074-33	Sequence 33, Appl
36	21.8	87.2	25	4	US-09-498-074-34	Sequence 34, Appl
37	21.8	87.2	25	4	US-09-498-074-35	Sequence 35, Appl
38	21.8	87.2	25	4	US-09-498-074-7	Sequence 6, Appl
39	21.8	87.2	25	4	US-09-498-074-8	Sequence 7, Appl
40	21.8	87.2	25	4	US-09-498-074-31	Sequence 8, Appl
41	21.8	87.2	25	4	US-09-498-074-32	Sequence 31, Appl
42	21.8	87.2	25	4	US-09-498-074-33	Sequence 32, Appl
43	21.8	87.2	25	4	US-09-498-074-34	Sequence 33, Appl
44	21.8	87.2	25	4	US-09-498-074-35	Sequence 34, Appl
45	21.8	87.2	25	4	US-09-498-074-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-09-233-493-6
; Sequence 6, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
US-09-233-493-6


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1  TITLE OF INVENTION: Recombination Sites
2
3  NUMBER OF SEQUENCES: 35
4
5  CORRESPONDENCE ADDRESS:
6
7  ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
8
9  STREET: 1100 New York Ave., N. W. Suite 600
10
11 CITY: Washington
12
13 STATE: DC
14
15 COUNTRY: USA
16
17 ZIP: 20005-3934
18
19 COMPUTER READABLE FORM:
20
21 MEDIUM TYPE: Floppy disk
22
23 COMPUTER: IBM PC compatible
24
25 OPERATING SYSTEM: PC-DOS/MS-DOS
26
27 SOFTWARE: Patentin Release #1.0, Version #1.30
28
29 CURRENT APPLICATION DATA:
30
31 APPLICATION NUMBER: US/09/005,476
32
33 FILING DATE: herewith
34
35 CLASSIFICATION:
36
37 PRIOR APPLICATION DATA:
38
39 APPLICATION NUMBER: 08/663,002
40
41 FILING DATE: 07-JUN-1996
42
43 TELECOMMUNICATION INFORMATION:
44
45 TELEPHONE: 202-371-2600
46
47 TELEFAX: 202-371-2540
48
49 INFORMATION FOR SEQ ID NO: 34:
50
51 SEQUENCE CHARACTERISTICS:
52
53 LENGTH: 25 base pairs
54
55 TYPE: nucleic acid
56
57 STRANDEDNESS: both
58
59 TOPOLOGY: both
60
61 MOLECULE TYPE: cdna
62
63 US-09-005-476-34

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Query Match 87.2%; Score 21.8; DB 3; Length 25;
Best Local Similarity 68.0%; Pred. No. 0.75;
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

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8	21.8	87.2	25	9	US-09-855-797A-60		Sequence 60, Appl
9	21.8	87.2	25	9	US-09-907-900-6		Sequence 6, Appli
10	21.8	87.2	25	9	US-09-907-900-7		Sequence 7, Appli
11	21.8	87.2	25	9	US-09-907-900-8		Sequence 8, Appli
12	21.8	87.2	25	9	US-09-907-900-40		Sequence 40, Appl

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RESULT 4
US-09-855-797A-6
; Sequence 6, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-6

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Query Match	87.2%	Score 21.8;	DB 9;	Length 25;
Best Local Similarity	68.0%	Pred. No. 3.8;		
Matches 17;	Conservative 8;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	1	AGCCTGCTTTTGTACAAACTGT	25	

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RESULT 5
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; Sequence 7, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
; US-09-855-797A-7

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Query Match          87.2%; Score 21.8; DB 9; Length 25;  
Best Local Similarity 68.0%; Pred.No.3.8;  
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
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Db 1 AGCCTGCTTCTTGTACAACTTGT 25

RESULT 6

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; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
US-09-855-797A-8

Query Match 87.2%; Score 21.8; DB 9; Length 25;
Best Local Similarity 68.0%; Pred. No. 3.8;
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASCCWGCTTTTTRTACWAASTKGW 25

Db 1 ACCCAGCTTCTTGTACAAAGTGGT 25

RESULT 7

US-09-855-797A-40
; Sequence 40, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
US-09-855-797A-40

Query Match 87.2%; Score 21.8; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASCCWGCTTTTTRTACWAASTKGW 25
Db 1 ASCCWGCTTTTTRTACWAASTKGW 25

RESULT 8

US-09-855-797A-60
; Sequence 60, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
US-09-855-797A-60

Query Match 87.2%; Score 21.8; DB 9; Length 25;
Best Local Similarity 68.0%; Pred. No. 3.8;
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASCCWGCTTTTTRTACWAASTKGW 25

Db 1 AGCCTGCTTTTATATACTACTTGA 25

RESULT 9

US-09-907-900-6
; Sequence 6, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
US-09-907-900-6

Query Match 87.2%; Score 21.8; DB 9; Length 25;
Best Local Similarity 68.0%; Pred. No. 3.8;

Matches	17;	Conservative	8;	Mismatches	0;	Indels	0;	Gaps	0;
---------	-----	--------------	----	------------	----	--------	----	------	----

Qy	1	ASCCWGCTT	Y	T	T	R	T	A	C	W	A	A	S	T	K	G	W	25
			:	:	:								:	:	:	:	:	
D _b	1	AGCCTGCTT <td>T <td>T <td>T <td>T <td>T <td>T <td>G <td>T <td>A <td>C <td>A <td>A <td>C <td>T <td>T <td>25</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	T <td>T <td>T <td>T <td>T <td>T <td>G <td>T <td>A <td>C <td>A <td>A <td>C <td>T <td>T <td>25</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td>	T <td>T <td>T <td>T <td>T <td>G <td>T <td>A <td>C <td>A <td>A <td>C <td>T <td>T <td>25</td> </td></td></td></td></td></td></td></td></td></td></td></td></td>	T <td>T <td>T <td>T <td>G <td>T <td>A <td>C <td>A <td>A <td>C <td>T <td>T <td>25</td> </td></td></td></td></td></td></td></td></td></td></td></td>	T <td>T <td>T <td>G <td>T <td>A <td>C <td>A <td>A <td>C <td>T <td>T <td>25</td> </td></td></td></td></td></td></td></td></td></td></td>	T <td>T <td>G <td>T <td>A <td>C <td>A <td>A <td>C <td>T <td>T <td>25</td> </td></td></td></td></td></td></td></td></td></td>	T <td>G <td>T <td>A <td>C <td>A <td>A <td>C <td>T <td>T <td>25</td> </td></td></td></td></td></td></td></td></td>	G <td>T <td>A <td>C <td>A <td>A <td>C <td>T <td>T <td>25</td> </td></td></td></td></td></td></td></td>	T <td>A <td>C <td>A <td>A <td>C <td>T <td>T <td>25</td> </td></td></td></td></td></td></td>	A <td>C <td>A <td>A <td>C <td>T <td>T <td>25</td> </td></td></td></td></td></td>	C <td>A <td>A <td>C <td>T <td>T <td>25</td> </td></td></td></td></td>	A <td>A <td>C <td>T <td>T <td>25</td> </td></td></td></td>	A <td>C <td>T <td>T <td>25</td> </td></td></td>	C <td>T <td>T <td>25</td> </td></td>	T <td>T <td>25</td> </td>	T <td>25</td>	25

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RESULT 10
US-09-907-900-7
; Sequence 7, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Braesch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombination Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-7

```

```

RESULT 11
US-09-907-900-8
; Sequence 8, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary P.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-8

```

Qy 1 ASCCWGCTTTTTRTACWAASTKGW 25
| : | : | : | : | : | : | : | :
Db 1 ACCCAGCTTCTTGTCAAAGTGGT 25

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RESULT 12
US-09-907-900-40
; Sequence 40, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-40

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RESULT 13
US-09-907-900-60
; Sequence 60, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-60

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Query Match	87.2%	Score 21.8;	DB 9;	Length 25;
Best Local Similarity	68.0%;	Pred. No. 3.8;		
Matches 17;	Conservative	8;	Mismatches	0;
Indels	0;	Gaps	0;	

Query Match 87.2%; Score 21.8; DB 9; Length 25;
Best Local Similarity 68.0%; Pred. No. 3.8;
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

DBb 1 AGCCTGCTTCTTGTACAAACTGT 25

RESULT 14

Query Match	87.2%	Score 21.8;	DB 9;	Length 25;
Best Local Similarity	68.0%	Pred. No. 3.8;		
Matches 17; Conservative	8;	Mismatches 0;	Indels 0;	Gaps 0;

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1  ASCCGCTTTTTRTACWAASTKGW 25
  ||:||:||:||:||:||:||:||
1  AGCCGCTTTTGTACAAACTGT 25

```

Query Match	87.2%	Score 21.8;	DB 9;	Length 25;
Best Local Similarity	68.0%;	Pred. No. 3.8;		
Matches 17;	Conservative	8;	Mismatches 0;	Indels 0;
Gaps 0;				

1 ASCCWGCTTYYTTRTACWAASTKGW 25

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:04 ; Search time 1532 Seconds
(without alignments)
594.643 Million cell updates/sec

Title: US-10-820-133-40
Perfect score: 25
Sequence: 1 ascwgcttctttacaaatkgw 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 segs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_hlc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gsl1.*
9: gb_gsl2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	21.8	87.2	79	7	CF651937	CF651937 24-L02016
2	21.8	87.2	80	6	CB394681	CB394681 OSTR142B1
3	21.8	87.2	83	6	CB398074	CB398074 OSTR197D3
4	21.8	87.2	83	6	CB401650	CB401650 OSTR197D3
5	21.8	87.2	87	7	CF652842	CF652842 80-L02016
6	21.8	87.2	89	7	CF651862	CF651862 19-L02052
7	21.8	87.2	89	7	CF652759	CF652759 75-L02013
8	21.8	87.2	89	7	CF653076	CF653076 94-L02016
9	21.8	87.2	93	7	CF652843	CF652843 80-L02016
10	21.8	87.2	95	7	CF651695	CF651695 07-L02052
11	21.8	87.2	95	7	CF651816	CF651816 16-L02057
12	21.8	87.2	95	7	CF651859	CF651859 19-L02036
13	21.8	87.2	95	7	CF651861	CF651861 19-L02052
14	21.8	87.2	95	7	CF651893	CF651893 21-L02052
15	21.8	87.2	95	7	CF651957	CF651957 25-L02036
16	21.8	87.2	95	7	CF651975	CF651975 26-L02036
17	21.8	87.2	95	7	CF652127	CF652127 35-L02057
18	21.8	87.2	95	7	CF652128	CF652128 35-L02057
19	21.8	87.2	95	7	CF652167	CF652167 38-L02036
20	21.8	87.2	95	7	CF652261	CF652261 44-L02036
21	21.8	87.2	95	7	CF652333	CF652333 49-L02013
22	21.8	87.2	95	7	CF652453	CF652453 56-L02052
23	21.8	87.2	95	7	CF652502	CF652502 59-L02052
24	21.8	87.2	95	7	CF652546	CF652546 62-L02036

25	21.8	87.2	95	7	CF652555	CF652555 62-L02057
26	21.8	87.2	95	7	CF652580	CF652580 64-L02036
27	21.8	87.2	95	7	CF652581	CF652581 64-L02036
28	21.8	87.2	95	7	CF652614	CF652614 66-L02036
29	21.8	87.2	95	7	CF652617	CF652617 66-L02052
30	21.8	87.2	95	7	CF652673	CF652673 69-L02058
31	21.8	87.2	95	7	CF652698	CF652698 71-L02036
32	21.8	87.2	95	7	CF652700	CF652700 71-L02052
33	21.8	87.2	95	7	CF652763	CF652763 75-L02035
34	21.8	87.2	95	7	CF652837	CF652837 79-L02057
35	21.8	87.2	95	7	CF652855	CF652855 80-L02058
36	21.8	87.2	95	7	CF652890	CF652890 83-L02013
37	21.8	87.2	95	7	CF652914	CF652914 84-L02036
38	21.8	87.2	95	7	CF652955	CF652955 86-L02057
39	21.8	87.2	95	7	CF652980	CF652980 88-L02052
40	21.8	87.2	95	7	CF653038	CF653038 92-L02013
41	21.8	87.2	95	7	CF653059	CF653059 93-L02035
42	21.8	87.2	95	7	CF653093	CF653093 95-L02036
43	21.8	87.2	95	7	CF653102	CF653102 95-L02058
c 44	21.8	87.2	99	6	CB396214	CB396214 OSTR168E7
45	21.8	87.2	99	7	CK587464	CK587464 IST_W15_3

ALIGNMENTS

RESULT 1
CF651937
LOCUS CF651937 79 bp mRNA linear EST 06-NOV-2003
DEFINITION 24-L020167-066-001-P06-SP6P MP1Z-ADIS-066 Arabidopsis thaliana cDNA clone MP1Zp2001P061Q 5-PRIME, mRNA sequence.
ACCESSION CF651937
VERSION CF651937
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 79)
AUTHORS Schmid, K.J., Soerensen, T.R., Stracke, R., Torjek, O., Altmann, T., Mitchell-Olds, T. and Weishaar, B.
TITLE Large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
JOURNAL Genome Res. 13 (6), 1250-1257 (2003)
MEDLINE 22683290
PUBMED 12799357
COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 79 Std Error: 0.00
Plate: 1 row: P column: 06
Seq primer: SP6P.
Location/Qualifiers
1..79
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecotype="Ws-0"
/db_xref="GABI:938525"
/db_xref="taxon:3702"
/clone="MP1Zp2001P061Q"
/tissue_type="root"
/lab_host="E. coli TOP10"
/note="Vector: pCMVSP01R6; Site 1: SalI; Site 2: NotI; cDNA library from Arabidopsis thaliana, accession Wasmilewskija-0; roots from three weeks old plants grown on MS-plates at 26M-OC with 16 hours light/day; library was made at the Max-Planck-Institute for Plant Breeding Research, Cologne, Germany; cloning sites SalI-NotI,

primer sites and orientation: SP6-Sali-CCAGCTCCG-Sprime-CDNA-polyA-CC-NotI-T7; GATEWAY compatible; Note: Sequencing granted in the context of the GABI Arabidopsis Verbund I: Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection' F1: Bernd Weishaar. Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>. This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further information."

ORIGIN

Query Match	87.2%	Score 21.8;	DB 7;	Length 79;
Best Local Similarity	68.0%;	Pred. No. 53;		
Matches	17;	Conservative	8;	Mismatches 0; Indels 0; Gaps 0;
QY	1	ASCCWGCCTTTTTRTACWAASTKGW	25	
db	48	ACCCAGCTTTCTTGTCACAAAGTGGT	72	

RESULT 2	CB394681/c	CB394681	80 bp	mRNA	linear	EST 15-MAY-2003
LOCUS		OSTR142812.1	AD-wrmcDNA	<i>Caenorhabditis elegans</i>	cDNA, mRNA sequence.	
DEFINITION		CB394681_				
ACCESSION		CB394681.1	GI:30736392			
VERSION						
KEYWORDS						
						EST.

SOURCE ORGANISM	REFERENCE	AUTHORS	TITLE
<i>Caenorhabditis elegans</i>	1 (bases 1 to 80)	Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Dresses, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tollas, P.P., Pkacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.	Complete genome annotation and resource for proteome-scale protein expression

JOURNAL COMMENT

Expression
Nat. Genet. (2003) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 859, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
POLY3=No.

FEATURES	Location/Qualifiers
source	1. .80
	/organism="Caenorhabditis elegans"
	/mol_type="mRNA"
	/strain="N2"
	/db_xref="taxon:6239"
	/sex="Hermaphrodite and male"
	/tissue_type="whole animal"
	/dev_stage="mixed stage"
	/clone_lib="AD-wrmcDNA"
	/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pC86"

ORIGIN

Query Match	87.2%	Score 21.8;	DB 6;	Length 80;
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subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

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Best Local Similarity 68.0%; Pred.No. 53;
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ASCCWGCTTTTTRTACWAASTKGW 25
| : | | | | : | : | : | : |
Db 55 ACCCAGCTTCTTGTCAAAAGTGT 31

RESULT 3	CB398074	CB398074	OSTR19703_1	AD-wrmCDNA	Caenorhabditis elegans	linear	83 bp	mRNA	EST 15-MAY-2003
LOCUS	CB398074	CB398074	AD-wrmCDNA	Caenorhabditis elegans	linear	83 bp	mRNA	EST 15-MAY-2003	
DEFINITION	CB398074	CB398074	AD-wrmCDNA	Caenorhabditis elegans	linear	83 bp	mRNA	EST 15-MAY-2003	
ACCESSION	CB398074	CB398074	AD-wrmCDNA	Caenorhabditis elegans	linear	83 bp	mRNA	EST 15-MAY-2003	
VERSION	CB398074.1	CB398074.1	AD-wrmCDNA	Caenorhabditis elegans	linear	83 bp	mRNA	EST 15-MAY-2003	
KEYWORDS	CB398074.1	CB398074.1	AD-wrmCDNA	Caenorhabditis elegans	linear	83 bp	mRNA	EST 15-MAY-2003	
EST.	CB398074.1	CB398074.1	AD-wrmCDNA	Caenorhabditis elegans	linear	83 bp	mRNA	EST 15-MAY-2003	
KEYWORDS	CB398074.1	CB398074.1	AD-wrmCDNA	Caenorhabditis elegans	linear	83 bp	mRNA	EST 15-MAY-2003	

SOURCE	Caenorhabditis elegans
ORGANISM	Caenorhabditis elegans
	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
	Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE	1 (bases 1 to 83)

AUTHORS Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevret, E., Papasotiropoulos, V., Tollas, P., Pracek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.

TITLE C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression

JOURNAL Nat. Genet. (2003) In press

COMMENT Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu
POLY#No.

FEATURES	Location/Qualifiers
source	1. 83
	/organism="Caenorhabditis elegans"
	/mol_type="mRNA"
	/strain="N2"
	/db_xref="taxon:6239"
	/sex="Hermaphrodite and male"
	/tissue_type="whole animal"
	/dev_stage="mixed stage"
	/clone_lib="AD-wrmcDNA"
	/note="The AD-wrmcDNA library was generated with poly(A) + RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPCR8"

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Query Match      87.2%; Score 21.8; DB 6; Length 83;
Best Local Similarity 68.0%; Pred. No. 53;
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY    1  ASCCWGCTTTTTRTACWAAASTKGW 25
       |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~
Db     33 AGCCTGCCTTTTTCGTACAAAATTGT 57

RESULT 4
CB401650/c
LOCUS      CB401650          83 bp      mRNA      linear      EST 15-MAY-2003
DEFINITION OSTF197D3_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION  CB401650

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Contact: Weisshaar B
ADIS DNA core facility at MPIZ


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/mol_type="mRNA"
/ecotype="Ws-0"
/db_xref="GABI:939685"
/db_xref="taxon:3702"
/cloned_lib="MP1ZP2001L233Q"
/tissue_type="root"
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/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from Arabidopsis thaliana, accession Wasselewskija-0; roots from three weeks old plants grown on MS-plates at 26M-OC with 16 hours light/day; library was made at the Max-Planck-Institute for Plant Breeding Research, Cologne, Germany; cloning sites Sali-NotI, primer sites and orientation: SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; GATEWAY compatible; Note: Sequencing granted in the context of the GABI Arabidopsis Verbund I; Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection' PI: Bernd Weisshaar Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further information."

ORIGIN
Query Match      87.2%; Score 21.8; DB 7; Length 89;
Best Local Similarity 68.0%; Pred. No. 54;
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY   1  ASCCGCTTTTTRTACWAASTKGW 25
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Db    44 ACCCAGCTTCTTGTCACAAAGTGT 68

RESULT 9
CF652843
LOCUS
DEFINITION
Arabidopsis thaliana (thale cress)
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T., Mitchell-Olds,T. and Weisshaar,B.
Large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
Genome Res. 13 (6), 1250-1257 (2003)
JOURNAL MEDLINE PUBMED
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
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Seq primer: SP6P; Location/Qualifiers
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/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from Arabidopsis thaliana, accession Wasselewskija-0; roots from three weeks old plants grown on MS-plates at 26M-OC with 16 hours light/day; library was made at the Max-Planck-Institute for Plant Breeding Research, Cologne, Germany; cloning sites Sali-NotI, primer sites and orientation: SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; GATEWAY compatible; Note: Sequencing granted in the context of the GABI Arabidopsis Verbund I; Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection' PI: Bernd Weisshaar Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further information."

ORIGIN
Query Match      87.2%; Score 21.8; DB 7; Length 89;
Best Local Similarity 68.0%; Pred. No. 54;
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY   1  ASCCGCTTTTTRTACWAASTKGW 25
      |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~
Db    44 ACCCAGCTTCTTGTCACAAAGTGT 68

RESULT 9
CF652843
LOCUS
DEFINITION
Arabidopsis thaliana (thale cress)
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T., Mitchell-Olds,T. and Weisshaar,B.
Large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
Genome Res. 13 (6), 1250-1257 (2003)
JOURNAL MEDLINE PUBMED
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 93 Std Error: 0.00
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Seq primer: SP6P; Location/Qualifiers
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/tissue_type="root"
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/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from Arabidopsis thaliana, accession Wasselewskija-0; roots from three weeks old plants grown on MS-plates at 26M-OC with 16 hours light/day; library was made at the Max-Planck-Institute for Plant Breeding Research, Cologne, Germany; cloning sites Sali-NotI, primer sites and orientation: SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; GATEWAY compatible; Note: Sequencing granted in the context of the GABI Arabidopsis Verbund I; Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection' PI: Bernd Weisshaar Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further information."

ORIGIN
Query Match      87.2%; Score 21.8; DB 7; Length 93;
Best Local Similarity 68.0%; Pred. No. 54;
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY   1  ASCCGCTTTTTRTACWAASTKGW 25
      |:|:~
Db    50 ACCCAGCTTCTTGTCACAAAGTGT 74

RESULT 10
CF651695
LOCUS
DEFINITION
Arabidopsis thaliana (thale cress)
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T., Mitchell-Olds,T. and Weisshaar,B.
Large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
Genome Res. 13 (6), 1250-1257 (2003)
JOURNAL MEDLINE PUBMED
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 95 Std Error: 0.00
Plate: 3 row: N column: 01
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/cloned_lib="MP1ZP-ADIS-066"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from Arabidopsis thaliana, accession Wasselewskija-0; roots from three weeks old plants grown on MS-plates at 26M-OC with 16 hours light/day; library was made at the Max-Planck-Institute for Plant Breeding Research, Cologne, Germany; cloning sites Sali-NotI, primer sites and orientation: SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; GATEWAY compatible; Note: Sequencing granted in the context of the GABI Arabidopsis Verbund I; Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection' PI: Bernd Weisshaar Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further information."

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detection' PI: Bernd Weisshaar Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de> This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further information."

ORIGIN

Query Match 87.2%; Score 21.8; DB 7; Length 95;
Best Local Similarity 68.0%; Pred. No. 55;
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

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Db 50 ACCGAGCTTCTTGTCACAAAGTGT 74

RESULT 13
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LOCUS
DEFINITION 19-L020523-066-003-E05-SP6P MP1Z-ADIS-066 Arabidopsis thaliana cDNA
clone MP1Zp2001E053Q 5-PRIME, mRNA sequence.

ACCESSION CF651861
VERSION CF651861.1 GI:37427806
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1 (bases 1 to 95)
AUTHORS Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T.,
Mitchell-Olds,T. and Weisshaar,B.

TITLE Large-scale identification and analysis of genome-wide
single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
JOURNAL Genome Res. 13 (6), 1250-1257 (2003)
MEDLINE 22683290
PUBMED 12799357

COMMENT Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weishaar@mpiz-koeln.mpg.de

Insert Length: 95 Std Error: 0.00

Plate: 3 row: E column: 05

Seq primer: SP6P;

Location/Qualifiers

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/lab_host="E. coli TOP10"

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/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from Arabidopsis thaliana, accession
Wasilewska-0; roots from three weeks old plants grown
on MS-plates at 26M-OC with 16 hours light/day; library
was made at the Max-Planck-Institute for Plant Breeding
Research, Cologne, Germany; cloning sites SalI-NotI,
primer sites and orientation:
SP6-SalI-CCACGCGCCG-5prime-cDNA-polyA-CC-NotI-T7; GATEWAY
compatible; Note: Sequencing granted in the context of the
GABI Arabidopsis Verbund I: Genetic Diversity,
'Establishment of high-efficiency SNP-based mapping tools
and development of methods for genome-wide mutation
detection' PI: Bernd Weisshaar Sequence submission managed
by RZPD/GABI-Primary database: <http://gabi.rzpd.de> This
clone is available from RZPD; contact RZPD (clone@rzpd.de)
for further information."

FEATURES

source

1. .95

/organism="Arabidopsis thaliana"

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/db_xref="taxon:3702"

/clone="MP1Zp2001E053Q"

/tissue_type="root"

/lab_host="E. coli TOP10"

/clone_lib="MP1Z-ADIS-066"

/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from Arabidopsis thaliana, accession
Wasilewska-0; roots from three weeks old plants grown
on MS-plates at 26M-OC with 16 hours light/day; library
was made at the Max-Planck-Institute for Plant Breeding
Research, Cologne, Germany; cloning sites SalI-NotI,
primer sites and orientation:
SP6-SalI-CCACGCGCCG-5prime-cDNA-polyA-CC-NotI-T7; GATEWAY
compatible; Note: Sequencing granted in the context of the
GABI Arabidopsis Verbund I: Genetic Diversity,
'Establishment of high-efficiency SNP-based mapping tools
and development of methods for genome-wide mutation
detection' PI: Bernd Weisshaar Sequence submission managed
by RZPD/GABI-Primary database: <http://gabi.rzpd.de> This
clone is available from RZPD; contact RZPD (clone@rzpd.de)
for further information."

ORIGIN

Query Match 87.2%; Score 21.8; DB 7; Length 95;
Best Local Similarity 68.0%; Pred. No. 55;
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

Query Match 87.2%; Score 21.8; DB 7; Length 95;
Best Local Similarity 68.0%; Pred. No. 55;
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASCCGCTTTTTRTACWAATKGM 25
|:|||||:|||||:|||||:|||||:
Db 50 ACCGAGCTTCTTGTCACAAAGTGT 74

RESULT 14
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DEFINITION 21-L020524-066-003-I06-SP6P MP1Z-ADIS-066 Arabidopsis thaliana cDNA
clone MP1Zp2001I063Q 5-PRIME, mRNA sequence.

ACCESSION CF651893
VERSION CF651893.1 GI:37427867
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1 (bases 1 to 95)
AUTHORS Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T.,
Mitchell-Olds,T. and Weisshaar,B.

TITLE Large-scale identification and analysis of genome-wide
single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
JOURNAL Genome Res. 13 (6), 1250-1257 (2003)
MEDLINE 22683290
PUBMED 12799357

COMMENT Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weishaar@mpiz-koeln.mpg.de

Insert Length: 95 Std Error: 0.00

Plate: 3 row: I column: 06

Seq primer: SP6P;

Location/Qualifiers

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/organism="Arabidopsis thaliana"

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/lab_host="E. coli TOP10"

/clone_lib="MP1Z-ADIS-066"

/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from Arabidopsis thaliana, accession
Wasilewska-0; roots from three weeks old plants grown
on MS-plates at 26M-OC with 16 hours light/day; library
was made at the Max-Planck-Institute for Plant Breeding
Research, Cologne, Germany; cloning sites SalI-NotI,
primer sites and orientation:
SP6-SalI-CCACGCGCCG-5prime-cDNA-polyA-CC-NotI-T7; GATEWAY
compatible; Note: Sequencing granted in the context of the
GABI Arabidopsis Verbund I: Genetic Diversity,
'Establishment of high-efficiency SNP-based mapping tools
and development of methods for genome-wide mutation
detection' PI: Bernd Weisshaar Sequence submission managed
by RZPD/GABI-Primary database: <http://gabi.rzpd.de> This
clone is available from RZPD; contact RZPD (clone@rzpd.de)
for further information."

FEATURES

source

1. .95

/organism="Arabidopsis thaliana"

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/ecotype="Ws-0"

/db_xref="GABI:938480"

/db_xref="taxon:3702"

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cDNA library from Arabidopsis thaliana, accession
Wasilewska-0; roots from three weeks old plants grown
on MS-plates at 26M-OC with 16 hours light/day; library
was made at the Max-Planck-Institute for Plant Breeding
Research, Cologne, Germany; cloning sites SalI-NotI,
primer sites and orientation:
SP6-SalI-CCACGCGCCG-5prime-cDNA-polyA-CC-NotI-T7; GATEWAY
compatible; Note: Sequencing granted in the context of the
GABI Arabidopsis Verbund I: Genetic Diversity,
'Establishment of high-efficiency SNP-based mapping tools
and development of methods for genome-wide mutation
detection' PI: Bernd Weisshaar Sequence submission managed
by RZPD/GABI-Primary database: <http://gabi.rzpd.de> This
clone is available from RZPD; contact RZPD (clone@rzpd.de)
for further information."

ORIGIN

Query Match 87.2%; Score 21.8; DB 7; Length 95;
Best Local Similarity 68.0%; Pred. No. 55;
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

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Query Match      87.2%; Score 21.8; DB 7; Length 95;
Best Local Similarity 68.0%; Pred.No.55;
Matches 17; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
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4	23	92.0	25	6	AR163183	Sequence
5	23	92.0	25	6	AR163184	Sequence
6	23	92.0	25	6	AR163185	Sequence
7	23	92.0	25	6	AR493784	Sequence
8	23	92.0	25	6	AR493785	Sequence
9	23	92.0	25	6	AR493786	Sequence
10	23	92.0	25	6	AX269138	Sequence
11	23	92.0	25	6	AX269139	Sequence
12	23	92.0	25	6	AX269140	Sequence
13	23	92.0	25	6	AX491651	Sequence
14	23	92.0	25	6	AX491652	Sequence
15	23	92.0	25	6	AX491653	Sequence
16	23	92.0	25	6	AX498622	Sequence
17	23	92.0	25	6	AX498623	Sequence
18	23	92.0	25	6	AX498624	Sequence
19	23	92.0	25	6	BD131338	Recombination

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:29:13 ; Search time 167.8 Seconds
(without alignments)
782.095 Million cell updates/sec

Title: US-10-820-133-41

Perfect score: 25
Sequence: 1 ascwgcttcttctacwaagttgg 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001as.*
5: Geneseq2001bs.*
6: Geneseq2002as.*
7: Geneseq2002bs.*
8: Geneseq2003as.*
9: Geneseq2003bs.*
10: Geneseq2003cs.*
11: Geneseq2003ds.*
12: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	92.0	25	AAT48221	attL1 cor
2	23	92.0	25	AAT48222	attL2 cor
3	23	92.0	25	AAT48223	attL3 cor
4	23	92.0	25	AAX78947	Oligonucl
5	23	92.0	25	AAX78975	Oligonucl
6	23	92.0	25	AAX78948	Oligonucl
7	23	92.0	25	AAX78946	Oligonucl
8	23	92.0	25	AAC87878	Escherich
9	23	92.0	25	AAC87879	Escherich
10	23	92.0	25	AAC87877	Escherich
11	23	92.0	25	AAX78948	Recombina
12	23	92.0	25	AAX78947	Recombina
13	23	92.0	25	AAX78946	Recombina
14	23	92.0	25	AAD14442	Recombina
15	23	92.0	25	AAD14440	Recombina
16	23	92.0	25	AAD14441	Recombina
17	23	92.0	25	AAS14787	Lambda ph
18	23	92.0	25	AAS14789	Lambda ph
19	23	92.0	25	AAS14788	Lambda ph
20	23	92.0	25	ABQ82125	Core sequ
21	23	92.0	25	ABQ82126	Core sequ

ALIGNMENTS

RESULT 1

AAT48221
ID AAT48221 standard; DNA; 25 BP.

AC AAT48221;

DT 20-OCT-1997 (first entry)

XX attL1 core region.

XX att recombination site; core region; mutation; enhance; recombination;
XX vector; subcloning; regulation; exchange; ss.

OS Synthetic.

PN WO9640724-A1.

PD 19-DEC-1996.

XX 07-JUN-1996; 96WO-US010082.

XX 07-JUN-1995; 95US-00486139.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA;

XX WPI; 1997-065168/06.

XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
XX using recombinant proteins and engineered recombination sites in vitro or
XX in vivo.

XX Claim 14; Page 56; 106pp; English.

XX AAT48210-25 are att recombination site core region DNA sequences. The
XX core region has at least one engineered mutation that enhances
XX recombination in vitro in the formation of a Cointegrate or Product DNA.
XX These core regions can be incorporated into novel vector donor DNA
XX molecules. The nucleic acids, vectors and methods of the invention are
XX used to obtain chimeric nucleic acid using recombination proteins and
XX engineered recombination sites in vitro or in vivo. The improved
XX specificity, speed and yields of the invention facilitates DNA or RNA
XX subcloning, regulation or exchange useful for any related purpose, e.g.

ABQ82124 Core sequ
ABT16632 Artificia
ABT16633 Artificia
ABT16631 Artificia
ACD28287 Nucleic a
ACD28288 Nucleic a
ACD28289 Nucleic a
ACD28488 Nucleic a
ACD28489 Nucleic a
ACD28487 Nucleic a
ADA38174 DNA of a
ADA38173 DNA of a
ADA38175 DNA of a
Ade0569 Core regi
Ade60571 Core regi
Ade60570 Core regi
Acc44663 Recombina
Acc44662 Recombina
Acc44661 Recombina
Adl93429 Recombina
Adl93427 Recombina
Adl93428 Recombina
Aas06176 Phage-lam
Aas06180 Phage-lam


```
XX PN WO9921977-A1.
XX PD 06-MAY-1999.
XX PF 26-OCT-1998; 98WO-US022589.
XX PR 24-OCT-1997; 97US-0065930P.
XX PR 23-OCT-1998; 98US-00177387.
XX PA (LIFE-) LIFE TECHNOLOGIES INC.
XX PI Hartley JL, Brasch MA, Temple GF, Fox DK;
XX DR WPI; 1999-303011/25.
XX PT New nucleic acid cloning methods.
XX PS Disclosure; Page 162; 185pp; English.
XX CC The invention relates to novel methods for cloning or subcloning one or
XX CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
XX CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
XX CC more desired nucleic acid segments flanked by at least 2 recombination
XX CC sites which do not recombine with each other; (2) one or more vector
XX CC donor molecules (VDMs) comprising at least 2 recombination sites which do
XX CC not recombine with each other; and (3) one or more site-specific
XX CC recombination proteins; (b) incubating the combination to transfer one or
XX CC more of the desired segments into one or more of the VDMs, thereby
XX CC producing one or more desired product molecules (PMs). The methods can be
XX CC used for the efficient and specific recombination of NAM segments. They
XX CC can be used to generate chimeric DNA or RNA molecules that have the
XX CC desired characteristics and/or nucleic acid segments. The methods can
XX CC also be used for changing vectors. The oligonucleotides AAX78935-X78994
XX CC are used in the method of the invention
XX SQ Sequence 25 BP; 5 A; 5 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 92.0%; Score 23; DB 2; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ASCCGCTTTTTRTACAAAGTTGG 25
Db 1 AGCCTGCTTCTTGACAAAGTTGG 25

RESULT 5
AAX78975
ID AAX78975 standard; DNA; 25 BP.
XX AC AAX78975;
XX DT 17-AUG-1999 (first entry)
XX DE Oligonucleotide #41 for recombination and cloning method.
XX KW Cloning; donor; recombination site; vector; chimeric; ss.
XX OS Synthetic.
XX PN WO9921977-A1.
XX PD 06-MAY-1999.
XX PF 26-OCT-1998; 98WO-US022589.
XX PR 24-OCT-1997; 97US-0065930P.
XX PR 23-OCT-1998; 98US-00177387.
XX PA (LIFE-) LIFE TECHNOLOGIES INC.
XX PI Hartley JL, Brasch MA, Temple GF, Fox DK;
XX DR WPI; 1999-303011/25.
XX PT New nucleic acid cloning methods.
XX PS Disclosure; Page 162; 185pp; English.
XX CC The invention relates to novel methods for cloning or subcloning one or
XX CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
XX CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
XX CC more desired nucleic acid segments flanked by at least 2 recombination
XX CC sites which do not recombine with each other; (2) one or more vector
XX CC donor molecules (VDMs) comprising at least 2 recombination sites which do
XX CC not recombine with each other; and (3) one or more site-specific
XX CC recombination proteins; (b) incubating the combination to transfer one or
XX CC more of the desired segments into one or more of the VDMs, thereby
XX CC producing one or more desired product molecules (PMs). The methods can be
XX CC used for the efficient and specific recombination of NAM segments. They
XX CC can be used to generate chimeric DNA or RNA molecules that have the
XX CC desired characteristics and/or nucleic acid segments. The methods can
XX CC also be used for changing vectors. The oligonucleotides AAX78935-X78994
XX CC are used in the method of the invention
XX SQ Sequence 25 BP; 5 A; 5 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 92.0%; Score 23; DB 2; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ASCCGCTTTTTRTACAAAGTTGG 25
Db 1 AGCCTGCTTCTTGACAAAGTTGG 25

RESULT 6
AAX78948
ID AAX78948 standard; DNA; 25 BP.
XX AC AAX78948;
XX DT 17-AUG-1999 (first entry)
XX DE Oligonucleotide #14 for recombination and cloning method.
XX KW Cloning; donor; recombination site; vector; chimeric; ss.
XX OS Synthetic.
XX PN WO9921977-A1.
XX PD 06-MAY-1999.
XX PF 26-OCT-1998; 98WO-US022589.
XX PR 24-OCT-1997; 97US-0065930P.
XX PR 23-OCT-1998; 98US-00177387.
XX PA (LIFE-) LIFE TECHNOLOGIES INC.
XX PI Hartley JL, Brasch MA, Temple GF, Fox DK;
XX DR WPI; 1999-303011/25.
XX PT New nucleic acid cloning methods.
XX PS Disclosure; Page 162; 185pp; English.
XX CC The invention relates to novel methods for cloning or subcloning one or
XX CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
XX CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
XX CC more desired nucleic acid segments flanked by at least 2 recombination
XX CC sites which do not recombine with each other; (2) one or more vector
XX CC donor molecules (VDMs) comprising at least 2 recombination sites which do
XX CC not recombine with each other; and (3) one or more site-specific
XX CC recombination proteins; (b) incubating the combination to transfer one or
XX CC more of the desired segments into one or more of the VDMs, thereby
XX CC producing one or more desired product molecules (PMs). The methods can be
XX CC used for the efficient and specific recombination of NAM segments. They
XX CC can be used to generate chimeric DNA or RNA molecules that have the
XX CC desired characteristics and/or nucleic acid segments. The methods can
XX CC also be used for changing vectors. The oligonucleotides AAX78935-X78994
XX CC are used in the method of the invention
XX SQ Sequence 25 BP; 4 A; 4 C; 4 G; 8 T; 0 U; 5 Other;
```



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RESULT 9
AAC87879
ID AAC87879 standard; DNA; 25 BP.
XX
AC AAC87879;
XX
DT 02-MAR-2001 (first entry)
XX
DE Escherichia coli core region recombinant site attL3 SEQ ID NO:14.
XX
KW Core region; recombination site; cloning; chimeric DNA; characteristic;
XX mutation; att site; lox site; ss.
XX
OS Escherichia coli.
XX
PN US6143557-A.
XX
PD 07-NOV-2000.
XX
PF 20-JAN-1999; 99US-00233493.
XX
PR 07-JUN-1995; 95US-00486139.
XX
PR 07-JUN-1996; 96US-00663002.
XX
PR 12-JAN-1998; 98US-00005476.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Brasch MA, Hartley JL;
XX
DR WPI; 2001-049004/06.
XX
PT Isolated nucleic acid molecules comprising a DNA segment having two
PT engineered recombination sites, derived from att or lox, which flank a
PT selectable marker and comprise a core region having an engineered
PT mutation.
XX
PS Claim 1; Col 18; 73pp; English.
XX
CC The present invention describes an isolated nucleic acid molecule (I)
CC comprising a first nucleic acid sequence having a defined sequence
CC (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,
CC or an RNA sequence corresponding to AAC87866 to AAC87881. Also described
CC are: (1) an isolated nucleic acid molecule (II) comprising a first
CC mutated recombination site that removes one or more stop codons from the
CC recombination site or avoids hairpin formation, the recombination site
CC being an att or lox site; (2) an isolated nucleic acid molecule (III)
CC comprising a first att recombination site comprising a mutation that
CC enhances recombination specificity; (3) vectors (IV) comprising the above
CC mentioned nucleic acid; and (4) cells comprising the above mentioned
CC nucleic acids or (IV). The nucleic acids are used in engineering a core
CC region of a given recombination site to provide mutative sites suitable
CC for subcloning reactions. The use of nucleic acids for obtaining
CC engineered recombination in vitro or in vivo makes the methods for DNA or
CC RNA subcloning, highly specific, rapid, and less labour intensive
XX
SQ Sequence 25 BP; 6 A; 6 C; 5 G; 8 T; 0 U; 0 Other;
Query Match 92.0%; Score 23; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Oy 1 ASCCGCTTTTTRTACAAAGTTGG 25
Db 1 ACCCAGCTTCTTGTACAAAGTTGG 25
RESULT 10
AAC87877
ID AAC87877 standard; DNA; 25 BP.
XX
AC AAC87877;
XX

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DT 02-MAR-2001 (first entry)
XX
DE Escherichia coli core region recombinant site attL1 SEQ ID NO:12.
XX
KW Core region; recombination site; cloning; chimeric DNA; characteristic;
XX mutation; att site; lox site; ss.
XX
OS Escherichia coli.
XX
PN US6143557-A.
XX
PD 07-NOV-2000.
XX
PF 20-JAN-1999; 99US-00233493.
XX
PR 07-JUN-1995; 95US-00486139.
XX
PR 07-JUN-1996; 96US-00663002.
XX
PR 12-JAN-1998; 98US-00005476.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Brasch MA, Hartley JL;
XX
DR WPI; 2001-049004/06.
XX
PT Isolated nucleic acid molecules comprising a DNA segment having two
PT engineered recombination sites, derived from att or lox, which flank a
PT selectable marker and comprise a core region having an engineered
PT mutation.
XX
PS Claim 1; Col 18; 73pp; English.
XX
CC The present invention describes an isolated nucleic acid molecule (I)
CC comprising a first nucleic acid sequence having a defined sequence
CC (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,
CC or an RNA sequence corresponding to AAC87866 to AAC87881. Also described
CC are: (1) an isolated nucleic acid molecule (II) comprising a first
CC mutated recombination site that removes one or more stop codons from the
CC recombination site or avoids hairpin formation, the recombination site
CC being an att or lox site; (2) an isolated nucleic acid molecule (III)
CC comprising a first att recombination site comprising a mutation that
CC enhances recombination specificity; (3) vectors (IV) comprising the above
CC mentioned nucleic acid; and (4) cells comprising the above mentioned
CC nucleic acids or (IV). The nucleic acids are used in engineering a core
CC region of a given recombination site to provide mutative sites suitable
CC for subcloning reactions. The use of nucleic acids for obtaining
CC engineered recombination in vitro or in vivo makes the methods for DNA or
CC RNA subcloning, highly specific, rapid, and less labour intensive
XX
SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 U; 0 Other;
Query Match 92.0%; Score 23; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Oy 1 ASCCGCTTTTTRTACAAAGTTGG 25
Db 1 AGCCTGCTTTTGTACAAAGTTGG 25
RESULT 11
AAF55748
ID AAF55748 standard; DNA; 25 BP.
XX
AC AAF55748;
XX
DT 12-APR-2001 (first entry)
XX
DE Recombination site attL3.
XX
KW Recombination site; cloning; att; ss.
XX
OS Unidentified.

```

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XX PN US6171861-B1.
XX XX
XX PD 09-JAN-2001.
XX PF
XX PF 12-JAN-1998; 98US-00005476.
XX PR 07-JUN-1995; 95US-00486139.
XX PR 07-JUN-1996; 96US-00663002.
XX PA (LIFE-) LIFE TECHNOLOGIES INC.
XX PI Hartley JL, Brasch MA;
XX PI WPI; 2001-136877/14.
XX DR
XX PT In vitro cloning of nucleic acid involves mixing vectors comprising
XX PT recombination sites and/or nucleic acid, incubating mixture to produce
XX PT chimeric molecule, contacting hosts with mixture and selecting host.
XX PS Claim 25; Col 46; 73pp; English.
XX CC The present invention relates to a method for in vitro cloning of a
XX CC nucleic acid of interest. The method involves mixing in vitro two vectors
XX CC each comprising at least one recombination site and the nucleic acid of
XX CC interest; incubating the mixture in the presence of at least one
XX CC recombination protein to result in recombination of the recombination
XX CC sites, leading to production of a chimeric nucleic acid molecule
XX CC comprising the nucleic acid of interest; contacting hosts with the
XX CC mixture; and selecting for a host comprising the chimeric nucleic acid
XX CC molecule; and selecting against a host comprising the vectors comprising
XX CC the second vector, to clone the nucleic acid. The present sequence is a
XX CC recombination site, which may be used in the method of the present
XX CC invention
XX SQ Sequence 25 BP; 5 A; 5 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 92.0%; Score 23; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASCCGCTTTTTRTACAAAGTTGG 25
Db 1 AGCTGCTTCTTGACAAAGTTGG 25

RESULT 13
AAF55746
ID AAF55746 standard; DNA; 25 BP.
XX AC
XX AC AAF55746;
XX DT 12-APR-2001 (first entry)
XX DE Recombination site attL1.
XX KW Recombination site; cloning; att; ss.
XX OS Unidentified.
XX PN US6171861-B1.
XX PD 09-JAN-2001.
XX PF 12-JAN-1998; 98US-00005476.
XX PR 07-JUN-1995; 95US-00486139.
XX PR 07-JUN-1996; 96US-00663002.
XX PA (LIFE-) LIFE TECHNOLOGIES INC.
XX PI Hartley JL, Brasch MA;
XX PI WPI; 2001-136877/14.
XX DR
XX PT In vitro cloning of nucleic acid involves mixing vectors comprising
XX PT recombination sites and/or nucleic acid, incubating mixture to produce
XX PT chimeric molecule, contacting hosts with mixture and selecting host.
XX PS Claim 25; Col 46; 73pp; English.
XX CC The present invention relates to a method for in vitro cloning of a
XX CC nucleic acid of interest. The method involves mixing in vitro two vectors
XX CC each comprising at least one recombination site and the nucleic acid of
XX CC interest; incubating the mixture in the presence of at least one
XX CC recombination protein to result in recombination of the recombination
XX CC sites, leading to production of a chimeric nucleic acid molecule
XX CC comprising the nucleic acid of interest; contacting hosts with the
XX CC mixture; and selecting for a host comprising the chimeric nucleic acid
XX CC molecule; and selecting against a host comprising the vectors comprising
XX CC the second vector, to clone the nucleic acid. The present sequence is a
XX CC recombination site, which may be used in the method of the present
XX CC invention
XX SQ Sequence 25 BP; 6 A; 6 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 92.0%; Score 23; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASCCGCTTTTTRTACAAAGTTGG 25
Db 1 ACCGAGCTTCTTGACAAAGTTGG 25

RESULT 12
AAF55747
ID AAF55747 standard; DNA; 25 BP.
XX AC
XX AC AAF55747;
XX DT 12-APR-2001 (first entry)
XX DE Recombination site attL2.
XX KW Recombination site; cloning; att; ss.
XX OS Unidentified.
XX PN US6171861-B1.
XX PD 09-JAN-2001.
XX PF 12-JAN-1998; 98US-00005476.
XX PR 07-JUN-1995; 95US-00486139.
XX PR 07-JUN-1996; 96US-00663002.
XX PA (LIFE-) LIFE TECHNOLOGIES INC.
XX PI Hartley JL, Brasch MA;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:19 ; Search time 35.9 Seconds
(without alignments)
494.978 Million cell updates/sec

Title: US-10-820-133-41

Perfect score: 25

Sequence: 1 ascwgctttrttacwaagtgg 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	23	92.0	25	3	US-09-233-493-13
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12	23	92.0	25	3	US-09-296-280-14
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14	23	92.0	25	4	US-09-498-074-12
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17	23	92.0	25	4	US-09-498-074-12
18	23	92.0	25	4	US-09-498-074-13
19	23	92.0	25	4	US-09-498-074-14
20	23	92.0	25	5	PCT-US96-10082A-12
21	23	92.0	25	5	PCT-US96-10082A-13
22	23	92.0	25	5	PCT-US96-10082A-14
23	23	92.0	228	4	US-09-107-532A-667
24	23	92.0	2408	1	US-08-486-013-69
25	23	92.0	2408	2	US-08-482-279-69
26	23	92.0	2408	2	US-08-342-268-69
27	23	92.0	2408	3	US-09-015-968-69

ALIGNMENTS

RESULT 1

US-09-233-493-12
; Sequence 12, Application US/09233493
; Patent No. 6143557

; GENERAL INFORMATION:

; APPLICANT: Hartley, James L.

; APPLICANT: Brasch, Michael A.

; TITLE OF INVENTION: Recombinational Cloning Using Engineered

; TITLE OF INVENTION: Recombination Sites

; NUMBER OF SEQUENCES: 35

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C

; STREET: 1100 New York Ave., N. W. Suite 600

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/233,493

; FILING DATE: 20-JAN-1999

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/005,476

; FILING DATE: 12-JAN-1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/663,002

; FILING DATE: 07-JUN-1996

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/486,139

; FILING DATE: 07-JUN-1995

; CLASSIFICATION:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-2600

; TELEFAX: 202-371-2540

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 25 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: both

; TOPOLOGY: both

; MOLECULE TYPE: cdna

US-09-233-493-12

Sequence 69, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 13, Appl
Sequence 19, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 40, Appl
Sequence 6, Appl
Sequence 7, Appl
Sequence 8, Appl
Sequence 11, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 31, Appl
Sequence 32, Appl

28 23 92.0 2408 3 US-09-397-386-69
29 23 92.0 3484 3 US-09-308-090-1
30 23 92.0 3484 4 US-09-380-090A-1
31 23 92.0 3757 2 US-09-016-366A-13
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33 23 92.0 5349 3 US-09-068-101-7
34 23 92.0 5349 4 US-09-970-921-7
35 23 92.0 5611 3 US-09-068-101-10
36 23 92.0 5611 4 US-09-970-921-10
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39 20.4 81.6 25 3 US-09-233-493-7
40 20.4 81.6 25 3 US-09-233-493-8
41 20.4 81.6 25 3 US-09-233-493-11
42 20.4 81.6 25 3 US-09-233-493-15
43 20.4 81.6 25 3 US-09-233-493-16
44 20.4 81.6 25 3 US-09-233-493-31
45 20.4 81.6 25 3 US-09-233-493-32


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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005.476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-12

Query Match          92.0%; Score 23; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 0.22;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASCCGCTTTTTRTACWAAGTTGG 25
   ||:|||||:||||:|||||
Db 1 AGCGTGCTTTTGTGACAAAGTTGG 25

RESULT 5
US-09-005-476-13
; Sequence 13, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005.476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-13

Query Match          92.0%; Score 23; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 0.22;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASCCGCTTTTTRTACWAAGTTGG 25
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Db 1 AGCGTGCTTTTGTGACAAAGTTGG 25

US-09-005-476-13
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Best Local Similarity 80.0%; Pred. No. 0.22;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
US-09-005-476-14
; Sequence 14, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005.476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-005-476-14

Query Match          92.0%; Score 23; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 0.22;
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; Sequence 12, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
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Result No.	Score	Query		DB	ID	Description
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2	23	92.0	25	9	US-09-855-797A-13	Sequence 13, Appl
3	23	92.0	25	9	US-09-855-797A-14	Sequence 14, Appl
4	23	92.0	25	9	US-09-855-797A-41	Sequence 41, Appl
5	23	92.0	25	9	US-09-855-797A-9	Sequence 9, Appl
6	23	92.0	25	9	US-09-822-634-9	Sequence 9, Appl
7	23	92.0	25	9	US-09-822-634-10	Sequence 10, Appl
8	23	92.0	25	9	US-09-822-634-11	Sequence 11, Appl
9	23	92.0	25	9	US-09-907-900-12	Sequence 12, Appl
10	23	92.0	25	9	US-09-907-900-13	Sequence 13, Appl
11	23	92.0	25	9	US-09-907-900-14	Sequence 14, Appl
12	23	92.0	25	9	US-09-907-900-41	Sequence 41, Appl
13	23	92.0	25	9	US-09-907-719-12	Sequence 12, Appl

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; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-719-14

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; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-719-41

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
594.643 Million cell updates/sec

Title: US-10-820-133-41
Perfect score: 25
Sequence: 1 accwgtttttrttacwaagttgg 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hic:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_g881:*
- 9: gb_g882:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 3	23	92.0	92	6	CB402537
C 4	23	92.0	94	6	CB402408
C 5	23	92.0	95	6	CB400591
C 6	23	92.0	95	6	CB401751
C 7	23	92.0	95	6	CB402238
C 8	23	92.0	97	6	CB401179
C 9	23	92.0	98	6	CB402581
C 10	23	92.0	100	6	CB392051
C 11	23	92.0	100	6	CB398867
C 12	23	92.0	100	6	CB398991
C 13	23	92.0	100	6	CB400512
C 14	23	92.0	102	6	CB392040
C 15	23	92.0	102	6	CB399013
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C 18	23	92.0	104	6	CB396275
C 19	23	92.0	106	6	CB396817
C 20	23	92.0	107	6	CB388456
C 21	23	92.0	108	6	CB398919
C 22	23	92.0	111	6	CB394444
C 23	23	92.0	111	6	CB395510
C 24	23	92.0	112	6	CB396297

C 25	23	92.0	112	6	CB397516	CB397516	OSTR191C6
C 26	23	92.0	112	6	CB398322	CB398322	OSTR202B1
C 27	23	92.0	118	6	CB396745	CB396745	OSTR177G3
C 28	23	92.0	120	6	CB392055	CB392055	OSTR163B1
C 29	23	92.0	120	6	CB400382	CB400382	OSTR175B7
C 30	23	92.0	121	6	CB392422	CB392422	OSTR099E7
C 31	23	92.0	121	6	CB399813	CB399813	OSTR163C2
C 32	23	92.0	126	6	CB400130	CB400130	OSTR169C5
C 33	23	92.0	128	6	CB400226	CB400226	OSTR171D4
C 34	23	92.0	128	6	CB401884	CB401884	OSTR202C5
C 35	23	92.0	129	6	CB401218	CB401218	OSTR191C6
C 36	23	92.0	141	6	CB388073	CB388073	OSTR091E1
C 37	23	92.0	190	6	CB396819	CB396819	OSTR179F1
C 38	23	92.0	225	6	CB397320	CB397320	OSTR186E2
C 39	23	92.0	227	6	CB398923	CB398923	OSTR212B6
C 40	23	92.0	227	6	CB398923	CB398923	OSTR212B6
C 41	23	92.0	247	6	CB401020	CB401020	OSTR186E2
C 42	23	92.0	247	6	CB401020	CB401020	OSTR186E2
C 43	23	92.0	262	6	CB395877	CB395877	OSTR163A3
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C 45	23	92.0	263	6	CB395890	CB395890	OSTR163C2

ALIGNMENTS

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LOCUS CB400039 87 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTR167D8_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB400039
VERSION CB400039.1 GI:30741766
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota: Metazoa, Nematoda: Chromadorea; Rhabditidae;
Rhabditoidea; Rhabditidae; Pelodierinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 87)
AUTHORS Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M.,
Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T.,
Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V.,
Tolia, P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
Nat. Genet. (2003) In press
JOURNAL Contact: Vidal M
COMMENT Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 859, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
POLYA=No..

FEATURES

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/mol_type="mRNA"
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/notes="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the

Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T.,
Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevet,E., Papasotirooulos,V.,
Tolias,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression

Nat. Genet. (2003) In press

Contact: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@fci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome

cloning project : Contact david_hill@fci.harvard.edu or

marc_vidal@fci.harvard.edu

POLYA=No.

FEATURES source

Location/Qualifiers

1. .94

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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"

ORIGIN

Query Match 92.0%; Score 23; DB 6; Length 94;

Best Local Similarity 80.0%; Pred. No. 16;

Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Db 32 ACCCAGCTTCTTGTCACAAAGTTGG 8

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DEFINITION OSTF179E7_1 AD-wrmcDNA Caenorhabditis elegans cdNA, linear EST 15-MAY-2003

ACCESSION CB400591

VERSION CB400591.1 GI:30742318

KEYWORDS EST.

SOURCE

ORGANISM

Caenorhabditis elegans

Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;

Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 95)

Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M.,

Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T.,

Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,

Endress,G.A., Jenna,S., Chevet,E., Papasotirooulos,V.,

Tolias,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,

Doucette-Stamm,L., Hill,D.E. and Vidal,M.

C. elegans ORFeome version 1.1: experimental verification of the

genome annotation and resource for proteome-scale protein

expression

Nat. Genet. (2003) In press

Contact: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@fci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome

cloning project : Contact david_hill@fci.harvard.edu or

marc_vidal@fci.harvard.edu

POLYA=No.

FEATURES source

Location/Qualifiers

1. .95

/organism="Caenorhabditis elegans"

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/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"

ORIGIN

Query Match 92.0%; Score 23; DB 6; Length 95;

Best Local Similarity 80.0%; Pred. No. 16;

Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Db 32 ACCCAGCTTCTTGTCACAAAGTTGG 8

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CB401751/c

LOCUS

DEFINITION OSTF198G7_1 AD-wrmcDNA Caenorhabditis elegans cdNA, linear EST 15-MAY-2003

ACCESSION CB401751

VERSION CB401751.1 GI:30743478

KEYWORDS EST.

SOURCE

ORGANISM

Caenorhabditis elegans

Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;

Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 95)

Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M.,

Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T.,

Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,

Endress,G.A., Jenna,S., Chevet,E., Papasotirooulos,V.,

Tolias,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,

Doucette-Stamm,L., Hill,D.E. and Vidal,M.

C. elegans ORFeome version 1.1: experimental verification of the

genome annotation and resource for proteome-scale protein

expression

Nat. Genet. (2003) In press

Contact: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@fci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were

designed on the predicted protein encoding ORF. C. elegans ORFeome

cloning project : Contact david_hill@fci.harvard.edu or

marc_vidal@fci.harvard.edu

POLYA=No.

FEATURES source

Location/Qualifiers

1. .95

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ACCESSION CB392040
VERSION   CB392040.1 GI:30733750
KEYWORDS EST.
SOURCE   Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida;
          Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE
AUTHORS Rebol,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M.,
         Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T.,
         Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
         Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V.,
         Tollias,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
         Doucette-Stamm,L., Hill,D.E. and Vidal,M.
TITLE    C. elegans ORPeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
JOURNAL Nat. Genet. (2003) In press
COMMENT  Contact: Vidal M
         Dana Farber Cancer Institute
         1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
         Tel: 617 632 5180
         Fax: 617 632 5739
         Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORPeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
POLYA=No.
LOCATION/Qualifiers
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        /note="The AD-wrmcDNA library was generated with poly(A)+
        RNA isolated from both hermaphrodite and male N2 worms of
        all larval stages, embryos, adults and dauers and the
        subsequent generation of cDNAs by poly(A) priming. The
        cDNAs were cloned into pPC86"

FEATURES
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Best Local Similarity 80.0%; Pred. No. 16;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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DB      49 AGCGTCGTTTTTTGTACAAAGTTGG 25

Search completed: November 16, 2004, 10:16:36
Job time : 1533 secs

ORIGIN

RESULT 15
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LOCUS   102 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTR213H5_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB399013
VERSION   CB399013.1 GI:30740740
KEYWORDS EST.
SOURCE   Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida;
          Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE
AUTHORS Rebol,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M.,
         Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T.,
         Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
         Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V.,
         Tollias,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
         Doucette-Stamm,L., Hill,D.E. and Vidal,M.
TITLE    C. elegans ORPeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
JOURNAL Nat. Genet. (2003) In press
COMMENT  Contact: Vidal M
         Dana Farber Cancer Institute
         1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
         Tel: 617 632 5180
         Fax: 617 632 5739
         Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORPeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
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LOCATION/Qualifiers
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FEATURES
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Best Local Similarity 80.0%; Pred. No. 16;
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DB      38 ACCCAGCTTCTTGACAAAGTTGG 14

ORIGIN

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:29:43 ; Search time 708.5 Seconds
(without alignments)
1668.656 Million cell updates/sec

Title: US-10-820-133-42
Perfect score: 25
Sequence: 1 gttcagcttctttacaaastkgw 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: gb_hcg.*
- 3: gb_in.*
- 4: gb_on.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22.6	90.4	25	6	AR124529 Sequence
2	22.6	90.4	25	6	AR124530 Sequence
3	22.6	90.4	25	6	AR163180 Sequence
4	22.6	90.4	25	6	AR163181 Sequence
5	22.6	90.4	25	6	AR493781 Sequence
6	22.6	90.4	25	6	AR493782 Sequence
7	22.6	90.4	25	6	AX491648 Sequence
8	22.6	90.4	25	6	AX491649 Sequence
9	22.6	90.4	25	6	AX498619 Sequence
10	22.6	90.4	25	6	AX498620 Sequence
11	22.6	90.4	25	6	AX787509 Sequence
12	22.6	90.4	25	6	AX787513 Sequence
13	22.6	90.4	25	6	BD131335 Recombina
14	22.6	90.4	25	6	BD131336 Recombina
15	22.6	90.4	25	6	BD131337 Recombina
16	22.6	90.4	25	6	BD131368 Recombina
17	22.6	90.4	27	6	AX787505 Sequence
18	22.6	90.4	35	6	AX684688 Sequence
19	22.6	90.4	37	6	CQ758822 Sequence

C 20	22.6	90.4	43	6	BD263259	Compositi
C 21	22.6	90.4	43	6	BD263260	Compositi
C 22	22.6	90.4	82	6	BD263456	Compositi
C 23	22.6	90.4	87	6	BD263465	Compositi
C 24	22.6	90.4	95	6	BD263452	Compositi
C 25	22.6	90.4	100	6	CQ758821	Sequence
C 26	22.6	90.4	102	6	BD263430	Compositi
C 27	22.6	90.4	102	6	BD263454	Compositi
C 28	22.6	90.4	102	6	BD263457	Compositi
C 29	22.6	90.4	102	6	BD263459	Compositi
C 30	22.6	90.4	102	6	BD263460	Compositi
C 31	22.6	90.4	102	6	BD263461	Compositi
C 32	22.6	90.4	102	6	BD263462	Compositi
C 33	22.6	90.4	120	6	BD263427	Compositi
C 34	22.6	90.4	125	6	BD263227	Compositi
C 35	22.6	90.4	125	6	AX787501	Sequence
C 36	22.6	90.4	135	6	BD263228	Compositi
C 37	22.6	90.4	153	6	BD263445	Compositi
C 38	22.6	90.4	153	6	BD263447	Compositi
C 39	22.6	90.4	153	6	BD263458	Compositi
C 40	22.6	90.4	204	6	BD263433	Compositi
C 41	22.6	90.4	204	6	BD263434	Compositi
C 42	22.6	90.4	204	6	BD263437	Compositi
C 43	22.6	90.4	204	6	BD263440	Compositi
C 44	22.6	90.4	255	6	BD263431	Compositi
C 45	22.6	90.4	255	6	BD263435	Compositi

ALIGNMENTS

RESULT 1	AR124529	Sequence 9 from patent US 6171861.	25 bp	DNA	linear	PAT 16-MAY-2001
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DEFINITION	Sequence 9 from patent US 6171861.					
ACCESSION	AR124529					
VERSION	AR124529.1	GI:14109890				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 25)					
AUTHORS	Hartley, J.L. and Brasch, M.A.					
TITLE	Recombinational cloning using engineered recombination sites					
JOURNAL	Patent: US 6171861-A 9 09-JAN-2001;					
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	: : : :					
Db	1 GTTCAGCTTTTGTGACAAACTTGT 25					
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LOCUS	AR124530					
DEFINITION	Sequence 10 from patent US 6171861.					
ACCESSION	AR124530					
VERSION	AR124530.1	GI:14109891				
KEYWORDS	.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	Unclassified.					
AUTHORS	1 (bases 1 to 25)					
TITLE	Hartley, J.L. and Brasch, M.A.					
	Recombinational cloning using engineered recombination sites					

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Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
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    |||||:||||:||||:||||:||||:
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RESULT 3
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LOCUS
DEFINITION Sequence 9 from patent US 6270969.
ACCESSION AR163180
VERSION AR163180.1 GI:16233689
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6270969-A 9 07-AUG-2001;
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Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4
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LOCUS
DEFINITION Sequence 10 from patent US 6270969.
ACCESSION AR163181
VERSION AR163181.1 GI:16233690
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6270969-A 10 07-AUG-2001;
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RESULT 5
AR493781 AR493781 25 bp mRNA linear PAT 15-MAY-2004
LOCUS
DEFINITION Sequence 9 from patent US 6720140.
ACCESSION AR493781
VERSION AR493781.1 GI:47266198
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6720140-A 9 13-APR-2004;
FEATURES Location/Qualifiers
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RESULT 6
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LOCUS
DEFINITION Sequence 10 from patent US 6720140.
ACCESSION AR493782
VERSION AR493782.1 GI:47266200
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6720140-A 10 13-APR-2004;
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RESULT 7
AX491648 AX491648 25 bp DNA linear PAT 16-AUG-2002
LOCUS
DEFINITION Sequence 9 from Patent EP1227147.
ACCESSION AX491648
VERSION AX491648.1 GI:22324156
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1227147-A 9 31-JUL-2002;
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    AUTHORS Hartley,J.L. and Brasch,M.A.
    TITLE Recombinational cloning using engineered recombination sites
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  SOURCE unidentified
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    AUTHORS Hartley,J.L. and Brasch,M.A.
    TITLE Recombinational cloning using engineered recombination sites
    JOURNAL Patent: EP 1229113-A 9 07-AUG-2002;
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  DEFINITION Sequence 10 from Patent EP1229113.
  ACCESSION AX498620
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  KEYWORDS
  SOURCE unidentified
  ORGANISM unidentified
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  REFERENCE
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    AUTHORS Hartley,J.L. and Brasch,M.A.
    TITLE Recombinational cloning using engineered recombination sites
    JOURNAL Patent: EP 1229113-A 10 07-AUG-2002;
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  VERSION AX787509.1 GI:32954583
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  SOURCE unidentified
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  REFERENCE
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    AUTHORS Nomura,N., Goshima,N., Kisu,Y. and Sono,S.
    TITLE Method for the preparation of nucleic acids
    JOURNAL Patent: WO 03044207-A 26 30-MAY-2003;
    Invitrogen Japan K.K. (JP) ; National Institute of Advanced
    Industrial Science and Technology (JP)
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VERSION AX787513.1 GI:32954587
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Nomura,N., Goshima,N., Kieu,Y. and Sono,S.
TITLE Method for the preparation of nucleic acids
JOURNAL Patent: WO 03044207-A 30 30-MAY-2003;
Industrial Science and Technology (JP)
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DEFINITION BD131335 25 bp DNA linear PAT 18-SEP-2002
sites.
ACCESSION BD131335
VERSION BD131335.1 GI:23226280
KEYWORDS JP 2002500861-A/9.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE Recombinational cloning using nucleic acids having recombination
JOURNAL Patent: JP 2002500861-A 9 15-JAN-2002;
LIFE TECHNOLOGIES INC
COMMENT OS Unknown
PN JP 2002500861-A/9
PD 15-JAN-2002
PR 26-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
JAMES L. HARTLEY, MICHAEL A. BRASCH, GARY F. TEMPLE, DONNA K. FOX PC
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RESULT 14
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sites.
ACCESSION BD131336
VERSION BD131336.1 GI:23226281
KEYWORDS JP 2002500861-A/10.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE Recombinational cloning using nucleic acids having recombination
JOURNAL Patent: JP 2002500861-A 10 15-JAN-2002;
LIFE TECHNOLOGIES INC
COMMENT OS Unknown
PN JP 2002500861-A/10
PD 15-JAN-2002
PR 26-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
JAMES L. HARTLEY, MICHAEL A. BRASCH, GARY F. TEMPLE, DONNA K. FOX PC
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ACCESSION BD131337
VERSION BD131337.1 GI:23226282
KEYWORDS JP 2002500861-A/11.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 25)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE Recombinational cloning using nucleic acids having recombination
JOURNAL Patent: JP 2002500861-A 11 15-JAN-2002;
LIFE TECHNOLOGIES INC
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PR 26-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
JAMES L. HARTLEY, MICHAEL A. BRASCH, GARY F. TEMPLE, DONNA K. FOX PC
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 90.4%; Score 22.6; DB 6; Length 25;
Best Local Similarity 76.0%; Pred. No. 42;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTCTTCTGTACAAAGTGGT 25
|||
Db 1 GTTCAGCTTCTTCTGTACAAAGTGGT 25

Search completed: November 16, 2004, 06:01:03
Job time : 708.5 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:29:13 ; Search time 167.8 Seconds
(without alignments)
782.095 Million cell updates/sec

Title: US-10-820-133-42

Perfect score: 25

Sequence: 1 gttcagcttcttctacaaatkgtw 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04.*
1: geneseqn1980s.*
2: geneseqn1990s.*
3: geneseqn2000s.*
4: geneseqn2001as.*
5: geneseqn2001bs.*
6: geneseqn2002as.*
7: geneseqn2002bs.*
8: geneseqn2003as.*
9: geneseqn2003bs.*
10: geneseqn2003cs.*
11: geneseqn2003ds.*
12: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22.6	90.4	25	2 AAT48219	Aat48219 attR2 cor
2	22.6	90.4	25	2 AAT48218	Aat48218 attR1 cor
3	22.6	90.4	25	2 AAX78944	Aax78944 Oligonucl
4	22.6	90.4	25	2 AAX78945	Aax78945 Oligonucl
5	22.6	90.4	25	2 AAX78976	Aax78976 Oligonucl
6	22.6	90.4	25	2 AAX78943	Aax78943 Oligonucl
7	22.6	90.4	25	4 AAS06181	Aas06181 Phage-lam
8	22.6	90.4	25	4 AAS06185	Aas06185 Phage-lam
9	22.6	90.4	25	4 AAC87875	Aac87875 Escherich
10	22.6	90.4	25	4 AAC87874	Aac87874 Escherich
11	22.6	90.4	25	4 AAF55744	Aaf55744 Recombina
12	22.6	90.4	25	4 AAF55743	Aaf55743 Recombina
13	22.6	90.4	25	4 AAD14437	Aad14437 Recombina
14	22.6	90.4	25	4 AAD14438	Aad14438 Recombina
15	22.6	90.4	25	6 ABQ82121	Abq82121 Core sequ
16	22.6	90.4	25	6 ABQ82122	Abq82122 Core sequ
17	22.6	90.4	25	8 ABT16628	Abt16628 Artificia
18	22.6	90.4	25	8 ABT16629	Abt16629 Artificia
19	22.6	90.4	25	9 ACD28284	Acd28284 Nucleic a
20	22.6	90.4	25	9 ACD28285	Acd28285 Nucleic a
21	22.6	90.4	25	9 ACD28485	Acd28485 Nucleic a

ALIGNMENTS

RESULT 1

AAT48219
ID AAT48219 standard; DNA; 25 BP.

XX AC AAT48219;

XX AC AAT48219;

DT 20-OCT-1997 (first entry)

XX DE attR2 core region.

XX att recombination site; core region; mutation; enhance; recombination;

XX vector; subcloning; regulation; exchange; ss.

XX OS Synthetic.

XX PN WO9640724-A1.

XX PD 19-DEC-1996.

XX PP 07-JUN-1996; 96WO-US010082.

XX PR 07-JUN-1995; 95US-00486139.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX PA Hartley JL, Brasch MA;

XX DR WPI; 1997-065168/06.

XX PT Nucleic acids, vectors and methods to obtain chimeric nucleic acid - using recombinant proteins and engineered recombination sites in vitro or in vivo.

XX PT Claim 14; Page 55; 106pp; English.

XX PS AAT48210-25 are att recombination site core region DNA sequences. The core region has at least one engineered mutation that enhances recombination in vitro in the formation of a Cointegrate or Product DNA. These core regions can be incorporated into novel vector donor DNA molecules. The nucleic acids, vectors and methods of the invention are used to obtain chimeric nucleic acid using recombination proteins and engineered recombination sites in vitro or in vivo. The improved specificity, speed and yields of the invention facilitates DNA or RNA subcloning, regulation or exchange useful for any related purpose, e.g.

22 ACD28484 Nucleic a
23 Acd38171 DNA of a
24 Acd38170 DNA of a
25 Acd60567 Core regi
26 Acd60566 Core regi
27 Abz58734 Att site
28 Abz58738 Att site
29 Acc59582 Nucleic a
30 Acc59578 Nucleic a
31 Acc44658 Recombina
32 Acc44659 Recombina
33 Adj46352 Wild type
34 Adj46356 Wild type
35 Adl93424 Recombina
36 Adl93425 Recombina
37 Ado06646 att recom
38 Ado06650 att recom
39 Adq48458 Bacteriop
40 Adq48454 Bacteriop
41 Aas06177 Phage-lam
42 Abz58730 Att site
43 Acc59574 Nucleic a
44 Adj46348 Wild type
45 Ado06642 att recom

CC in vitro recombination of DNA segments, and in vitro or in vivo insertion
CC or modification of transcribed, replicated, isolated or genomic DNA or
XX RNA

SQ Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 U; 0 Other;

Query Match 90.4%; Score 22.6; DB 2; Length 25;

Best Local Similarity 76.0%; Pred. No. 4.9;

Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTTRTACWAATKGM 25

Db 1 GTTCAGCTTTTCTGTACAACTTGT 25

RESULT 2

AAT48218

ID AAT48218 standard; DNA; 25 BP.

XX AC

AAT48218;

DT 20-OCT-1997 (first entry)

XX DE

attR1 core region.

KW att recombination site; core region; mutation; enhance; recombination;

KW vector; subcloning; regulation; exchange; ss.

XX OS

Synthetic.

XX PN

WO9640724-A1.

XX PD

19-DEC-1996.

XX PF

07-JUN-1996; 96WO-US010082.

XX PR

07-JUN-1995; 95US-00486139.

XX PA

(LIFE-) LIFE TECHNOLOGIES INC.

XX PI

Hartley JL, Brasch MA;

XX DR

WPI; 1997-065168/06.

XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -

PT using recombinant proteins and engineered recombination sites in vitro or

PT in vivo.

XX PS

Claim 14; Page 55; 106pp; English.

XX SQ

AAT48210-25 are att recombination site core region DNA sequences. The

CC core region has at least one engineered mutation that enhances

CC recombination in vitro in the formation of a Cointegrate or Product DNA.

CC These core regions can be incorporated into novel vector donor DNA

CC molecules. The nucleic acids, vectors and methods of the invention are

CC used to obtain chimeric nucleic acid using recombination proteins and

CC engineered recombination sites in vitro or in vivo. The improved

CC specificity, speed and yields of the invention facilitates DNA or RNA

CC subcloning, regulation or exchange useful for any related purpose, e.g.

CC in vitro recombination of DNA segments, and in vitro or in vivo insertion

CC or modification of transcribed, replicated, isolated or genomic DNA or

XX RNA

SQ Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 U; 0 Other;

Query Match 90.4%; Score 22.6; DB 2; Length 25;

Best Local Similarity 76.0%; Pred. No. 4.9;

Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTTRTACWAATKGM 25

Db 1 GTTCAGCTTTTCTGTACAACTTGT 25

RESULT 3

AAX78944

ID AAX78944 standard; DNA; 25 BP.

XX AC

AAX78944;

DT 17-AUG-1999 (first entry)

XX DE

Oligonucleotide #10 for recombination and cloning method.

KW Cloning; donor; recombination site; vector; chimeric; ss.

XX OS

Synthetic.

XX PN

WO9921977-A1.

XX PD

06-MAY-1999.

XX PF

26-OCT-1998; 98WO-US022589.

XX PR

24-OCT-1997; 97US-0065930P.

XX PR

23-OCT-1998; 98US-00177387.

XX PA

(LIFE-) LIFE TECHNOLOGIES INC.

XX PI

Hartley JL, Brasch MA, Temple GF, Fox DK;

XX DR

WPI; 1999-303011/25.

XX New nucleic acid cloning methods.

XX Disclosure; Page 161; 185pp; English.

XX The invention relates to novel methods for cloning or subcloning one or more nucleic acid molecules (NMs) comprising: (a) combining in vitro or in vivo: (1) at least one insert donor molecules (IDMs) comprising one or more desired nucleic acid segments flanked by at least 2 recombination sites which do not recombine with each other; (2) one or more vector donor molecules (VDMs) comprising at least 2 recombination sites which do not recombine with each other; and (3) one or more site-specific recombination proteins; (b) incubating the combination to transfer one or more of the desired segments into one or more of the VDMs, thereby can be producing one or more desired product molecules (PMs). The methods can be used for the efficient and specific recombination of NAM segments. They can be used to generate chimeric DNA or RNA molecules that have the desired characteristics and/or nucleic acid segments. The methods can also be used for changing vectors. The oligonucleotides AAX78935-X78994 are used in the method of the invention

SQ Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 U; 0 Other;

Query Match 90.4%; Score 22.6; DB 2; Length 25;

Best Local Similarity 76.0%; Pred. No. 4.9;

Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTTRTACWAATKGM 25

Db 1 GTTCAGCTTTTCTGTACAACTTGT 25

RESULT 4

AAX78945

ID AAX78945 standard; DNA; 25 BP.

XX AC

AAX78945;

DT 17-AUG-1999 (first entry)

XX DE

Oligonucleotide #11 for recombination and cloning method.

KW Cloning; donor; recombination site; vector; chimeric; ss.

XX

CC donor molecules (VDMs) comprising at least 2 recombination sites which do
 CC not recombine with each other; and (3) one or more site-specific
 CC recombination proteins; (b) incubating the combination to transfer one or
 CC more of the desired segments into one or more of the VDMs, thereby
 CC producing one or more desired product molecules (Pwms). The methods can be
 CC used for the efficient and specific recombination of NAM segments. They
 CC can be used to generate chimeric DNA or RNA molecules that have the
 CC desired characteristics and/or nucleic acid segments. The methods can
 CC also be used for changing vectors. The oligonucleotides AAX78935-X78994
 CC are used in the method of the invention

XX SQ Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 U; 0 Other;

Query Match 90.4%; Score 22.6; DB 2; Length 25;
 Best Local Similarity 76.0%; Pred. No. 4.9;
 Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAASTKGW 25
 Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 7

AAS06181
 ID AAS06181 standard; DNA; 25 BP.

XX AC AAS06181;

XX DT 12-SEP-2001 (first entry)

XX DE Phage-lambda recombination site attR1.

XX KW Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
 XX KW lambda integrase; therapeutic; ss.

XX OS Bacteriophage lambda.

XX PN WO200142509-A1.

XX PD 14-JUN-2001.

XX PF 11-DEC-2000; 2000WO-US033546.

XX PR 10-DEC-1999; 99US-0169983P.

XX PR 09-MAR-2000; 2000US-0188020P.

XX PA (CHEO/) CHEO D.

XX PA (BRAS/) BRASCH M A.

XX PA (TEMP/) TEMPLE G F.

XX PA (HART/) HARTLEY J L.

XX PA (BYRD/) BYRD D R N.

XX PI Cheo D, Brasch MA, Temple GF, Hartley JL, Byrd DRN;

XX WPI; 2001-356174/37.

XX DR Producing hybrid nucleic acids, useful for expressing novel therapeutic
 XX PT polypeptides, by mixing the same or different nucleic acids having one or
 XX PT more recombination sites in the presence of recombination proteins, e.g.
 XX PT Cre.

XX PS Disclosure; Fig 24A; 357pp; English.

XX SS AAS06174-AAS06322 represent Bacteriophage lambda att recombination site
 CC nucleic acid sequences, and PCR primers of the invention. The att
 CC sequences are recognised by the recombination protein lambda integrase
 CC (Int). The invention is a new method of producing a population of hybrid
 CC nucleic acids comprising mixing at least a first population of nucleic
 CC acids comprising one or more recombination sites with at least one target
 CC nucleic acid comprising one or more recombination sites and causing some
 CC or all of the nucleic acids to recombine with all or some of the target
 CC nucleic acids. The method is useful for producing a population of hybrid
 CC nucleic acids which may be the same or different. The nucleic acids may

CC be used to express therapeutic proteins or peptides and they may also be
 CC linked to create novel fusion proteins by expressing different sequences
 CC linked to each other. The method allows simultaneous cloning of two or
 CC more different nucleic acids

XX SQ Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 U; 0 Other;

Query Match 90.4%; Score 22.6; DB 4; Length 25;
 Best Local Similarity 76.0%; Pred. No. 4.9;
 Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAASTKGW 25
 Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 8

AAS06185
 ID AAS06185 standard; DNA; 25 BP.

XX AC AAS06185;

XX DT 12-SEP-2001 (first entry)

XX DE Phage-lambda recombination site attR2.

XX KW Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
 XX KW lambda integrase; therapeutic; ss.

XX OS Bacteriophage lambda.

XX PN WO200142509-A1.

XX PD 14-JUN-2001.

XX PF 11-DEC-2000; 2000WO-US033546.

XX PR 10-DEC-1999; 99US-0169983P.

XX PR 09-MAR-2000; 2000US-0188020P.

XX PA (CHEO/) CHEO D.

XX PA (BRAS/) BRASCH M A.

XX PA (TEMP/) TEMPLE G F.

XX PA (HART/) HARTLEY J L.

XX PA (BYRD/) BYRD D R N.

XX PI Cheo D, Brasch MA, Temple GF, Hartley JL, Byrd DRN;

XX WPI; 2001-356174/37.

XX DR Producing hybrid nucleic acids, useful for expressing novel therapeutic
 XX PT polypeptides, by mixing the same or different nucleic acids having one or
 XX PT more recombination sites in the presence of recombination proteins, e.g.
 XX PT Cre.

XX PS Disclosure; Fig 24A; 357pp; English.

XX SS AAS06174-AAS06322 represent Bacteriophage lambda att recombination site
 CC nucleic acid sequences, and PCR primers of the invention. The att
 CC sequences are recognised by the recombination protein lambda integrase
 CC (Int). The invention is a new method of producing a population of nucleic
 CC acids comprising mixing at least a first population of nucleic
 CC acids comprising one or more recombination sites with at least one target
 CC nucleic acid comprising one or more recombination sites and causing some
 CC or all of the nucleic acids to recombine with all or some of the target
 CC nucleic acids. The method is useful for producing a population of hybrid
 CC nucleic acids which may be the same or different. The nucleic acids may
 CC be used to express therapeutic proteins or peptides and they may also be
 CC used to create novel fusion proteins by expressing different sequences
 CC linked to each other. The method allows simultaneous cloning of two or
 CC more different nucleic acids

XX SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 U; 0 Other;

```

Query Match      90.4%; Score 22.6; DB 4; Length 25;
Best Local Similarity 76.0%; Pred. No. 4.9;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTTRTACWAATKGM 25
DB 1 GTTCAGCTTTTCTGTACAACTTGT 25

RESULT 9
AAC87875
ID AAC87875 standard; DNA; 25 BP.
XX AAC87875;
XX
XX
XX 02-MAR-2001 (first entry)
XX Escherichia coli core region recombinant site attr2 SEQ ID NO:10.
XX Core region; recombination site; cloning; chimeric DNA; characteristic;
XX mutation; att site; lox site; ss.
XX Escherichia coli.
XX US6143557-A.
XX 07-NOV-2000.
XX 20-JAN-1999; 99US-00233493.
XX 07-JUN-1995; 95US-00486139.
XX 07-JUN-1996; 96US-00663002.
XX 12-JAN-1998; 98US-00005476.
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX Brasch MA, Hartley JL;
XX WPI; 2001-049004/06.
XX Isolated nucleic acid molecules comprising a DNA segment having two
XX engineered recombination sites, derived from att or lox, which flank a
XX selectable marker and comprise a core region having an engineered
XX mutation.
XX Claim 1; Col 18; 73pp; English.
XX The present invention describes an isolated nucleic acid molecule (I)
XX comprising a first nucleic acid sequence having a defined sequence
XX (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,
XX or an RNA sequence corresponding to AAC87866 to AAC87881. Also described
XX are: (1) an isolated nucleic acid molecule (II) comprising a first
XX mutated recombination site that removes one or more stop codons from the
XX recombination site or avoids hairpin formation, the recombination site
XX being an att or lox site; (2) an isolated nucleic acid molecule (III)
XX comprising a first att recombination site comprising a mutation that
XX enhances recombination specificity; (3) vectors (IV) comprising the above
XX mentioned nucleic acids; and (4) cells comprising the above mentioned
XX nucleic acids or (IV). The nucleic acids are used in engineering a core
XX region of a given recombination site to provide mutative sites suitable
XX for subcloning reactions. The use of nucleic acids for obtaining
XX engineered recombination in vitro or in vivo makes the methods for DNA or
XX RNA subcloning, highly specific, rapid, and less labour intensive
XX Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 U; 0 Other;

Query Match      90.4%; Score 22.6; DB 4; Length 25;
Best Local Similarity 76.0%; Pred. No. 4.9;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTTRTACWAATKGM 25
DB 1 GTTCAGCTTTTCTGTACAACTTGT 25

RESULT 11
AAF55744
ID AAF55744 standard; DNA; 25 BP.
XX

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DB 1 GTTCAGCTTTTCTGTACAACTTGT 25

RESULT 10
AAC87874
ID AAC87874 standard; DNA; 25 BP.
XX AAC87874;
XX
XX 02-MAR-2001 (first entry)
XX Escherichia coli core region recombinant site attr1 SEQ ID NO:9.
XX Core region; recombination site; cloning; chimeric DNA; characteristic;
XX mutation; att site; lox site; ss.
XX Escherichia coli.
XX US6143557-A.
XX 07-NOV-2000.
XX 20-JAN-1999; 99US-00233493.
XX 07-JUN-1995; 95US-00486139.
XX 07-JUN-1996; 96US-00663002.
XX 12-JAN-1998; 98US-00005476.
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX Brasch MA, Hartley JL;
XX WPI; 2001-049004/06.
XX Isolated nucleic acid molecules comprising a DNA segment having two
XX engineered recombination sites, derived from att or lox, which flank a
XX selectable marker and comprise a core region having an engineered
XX mutation.
XX Claim 1; Col 18; 73pp; English.
XX The present invention describes an isolated nucleic acid molecule (I)
XX comprising a first nucleic acid sequence having a defined sequence
XX (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,
XX or an RNA sequence corresponding to AAC87866 to AAC87881. Also described
XX are: (1) an isolated nucleic acid molecule (II) comprising a first
XX mutated recombination site that removes one or more stop codons from the
XX recombination site or avoids hairpin formation, the recombination site
XX being an att or lox site; (2) an isolated nucleic acid molecule (III)
XX comprising a first att recombination site comprising a mutation that
XX enhances recombination specificity; (3) vectors (IV) comprising the above
XX mentioned nucleic acids; and (4) cells comprising the above mentioned
XX nucleic acids or (IV). The nucleic acids are used in engineering a core
XX region of a given recombination site to provide mutative sites suitable
XX for subcloning reactions. The use of nucleic acids for obtaining
XX engineered recombination in vitro or in vivo makes the methods for DNA or
XX RNA subcloning, highly specific, rapid, and less labour intensive
XX Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 U; 0 Other;

Query Match      90.4%; Score 22.6; DB 4; Length 25;
Best Local Similarity 76.0%; Pred. No. 4.9;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTTRTACWAATKGM 25
DB 1 GTTCAGCTTTTCTGTACAACTTGT 25

RESULT 11
AAF55744
ID AAF55744 standard; DNA; 25 BP.
XX

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```

AC AAF55744;
DT 12-APR-2001 (first entry)
XX Recombination site attR2.
DE Recombination site; cloning; att; ss.
XX Unidentified.
XX US6171861-B1.
PN 09-JAN-2001.
XX 12-JAN-1998; 98US-00005476.
XX 07-JUN-1995; 95US-00486139.
PR 07-JUN-1996; 96US-00663002.
XX (LIFE-) LIFE TECHNOLOGIES INC.
PA Hartley JL, Brasch MA;
PI WPI; 2001-136877/14.
XX In vitro cloning of nucleic acid involves mixing vectors comprising
PT recombination sites and/or nucleic acid, incubating mixture to produce
PT chimeric molecule, contacting hosts with mixture and selecting host.
XX Claim 25; Col 46; 73pp; English.
CC The present invention relates to a method for in vitro cloning of a
CC nucleic acid of interest. The method involves mixing in vitro two vectors
CC each comprising at least one recombination site and the nucleic acid of
CC interest; incubating the mixture in the presence of at least one
CC recombination protein to result in recombination of the recombination
CC sites, leading to production of a chimeric nucleic acid molecule
CC comprising the nucleic acid of interest; contacting hosts with the
CC mixture; and selecting for a host comprising the chimeric nucleic acid
CC molecule, and selecting against a host comprising the vectors comprising
CC the second vector, to clone the nucleic acid. The present sequence is a
CC recombination site, which may be used in the method of the present
XX invention
XX Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 U; 0 Other;
SQ
CC Query Match 90.4%; Score 22.6; DB 4; Length 25;
CC Best Local Similarity 76.0%; Pred. No. 4.9;
CC Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
CC
OY 1 GTTCAGCTTCTTCTACAACTGT 25
DB 1 GTTCAGCTTCTTCTACAACTGT 25
RESULT 12
AAF55743
ID AAF55743 standard; DNA; 25 BP.
AC AAF55743;
XX
XX 12-APR-2001 (first entry)
DT Recombination site attR1.
DE Recombination site; cloning; att; ss.
XX Unidentified.
XX US6171861-B1.
PN 09-JAN-2001.
XX
XX Query Match 90.4%; Score 22.6; DB 4; Length 25;
XX Best Local Similarity 76.0%; Pred. No. 4.9;
XX Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 GTTCAGCTTCTTCTACAACTGT 25
DB 1 GTTCAGCTTCTTCTACAACTGT 25
RESULT 13
AAD14437
ID AAD14437 standard; DNA; 25 BP.
AC AAD14437;
XX
XX 01-NOV-2001 (first entry)
DT Recombination site attB3 DNA.
DE Recombination site; copy number; replicon; recombinatorial cloning;
XX attB3; ds.
XX Unidentified.
XX US6270969-B1.
PN 07-AUG-2001.
XX
XX 20-JAN-1999; 99US-00233492.
PF
XX 07-JUN-1995; 95US-00486139.
PR 07-JUN-1996; 96US-00663002.
XX
XX (INVI-) INVITROGEN CORP.
PA Hartley JL, Brasch MA;
PI WPI; 2001-488248/53.
XX
XX Methods for apposing nucleic acids comprising an expression signal and a
PT gene/partial gene, using recombinatorial cloning by incubating the

```


CC acid sequences. The vectors can also be used to convert a DNA fragment
CC into an inverted repeat structure. Plants transformed with a vector from
CC the present invention can be used in a conventional breeding scheme to
CC produce more plants with the same characteristics or to introduce a
CC chimeric gene for reduction of the phenotypic expression of nucleic
CC acids. The present sequence represents the core sequence of recombination
CC site attB1 which is given in the exemplification of the present invention
XX

SQ Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 U; 0 Other;

Query Match 90.4%; Score 22.6; DB 6; Length 25;
Best Local Similarity 76.0%; Pred. No. 4.9;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAASTKGW 25

Db 1 GTTCAGCTTTTGTACAAACTTGT 25

Search completed: November 16, 2004, 04:02:49
Job time : 167.8 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:19 , Search time 35.9 Seconds
(without alignments)
494.978 Million cell updates/sec

Title: US-10-820-133-42
Perfect score: 25
Sequence: 1 gttcagcttcttttacwaaatkgw 25

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22.6	90.4	25	3	US-09-233-493-9
2	22.6	90.4	25	3	US-09-233-493-10
3	22.6	90.4	25	3	US-09-005-476-9
4	22.6	90.4	25	3	US-09-005-476-10
5	22.6	90.4	25	3	US-09-233-492-9
6	22.6	90.4	25	3	US-09-233-492-10
7	22.6	90.4	25	3	US-09-296-280-9
8	22.6	90.4	25	3	US-09-296-280-10
9	22.6	90.4	25	3	US-09-296-280-11
10	22.6	90.4	25	3	US-09-296-280-42
11	22.6	90.4	25	4	US-09-498-074-9
12	22.6	90.4	25	4	US-09-498-074-10
13	22.6	90.4	25	4	US-09-498-074-9
14	22.6	90.4	25	4	US-09-498-074-10
15	22.6	90.4	25	5	PCT-US96-10082A-9
16	22.6	90.4	25	5	PCT-US96-10082A-10
17	22	88.0	25	3	US-09-233-493-11
18	22	88.0	25	3	US-09-233-493-15
19	22	88.0	25	3	US-09-233-493-16
20	22	88.0	25	3	US-09-005-476-11
21	22	88.0	25	3	US-09-005-476-15
22	22	88.0	25	3	US-09-005-476-16
23	22	88.0	25	3	US-09-233-492-11
24	22	88.0	25	3	US-09-233-492-15
25	22	88.0	25	3	US-09-233-492-16
26	22	88.0	25	3	US-09-296-280-15
27	22	88.0	25	3	US-09-296-280-16

28	22	88.0	25	3	US-09-296-280-43	Sequence 43, Appl
29	22	88.0	25	4	US-09-498-074-11	Sequence 11, Appl
30	22	88.0	25	4	US-09-498-074-15	Sequence 15, Appl
31	22	88.0	25	4	US-09-498-074-16	Sequence 16, Appl
32	22	88.0	25	4	US-09-498-074-11	Sequence 11, Appl
33	22	88.0	25	4	US-09-498-074-15	Sequence 15, Appl
34	22	88.0	25	4	US-09-498-074-16	Sequence 16, Appl
35	22	88.0	25	5	PCT-US96-10082A-11	Sequence 11, Appl
36	22	88.0	25	5	PCT-US96-10082A-15	Sequence 15, Appl
37	22	88.0	25	5	PCT-US96-10082A-16	Sequence 16, Appl
38	22	88.0	201	1	US-08-021-667A-18	Sequence 18, Appl
39	22	88.0	201	1	US-08-410-544-18	Sequence 18, Appl
40	22	88.0	201	1	US-08-728-785A-18	Sequence 18, Appl
41	22	88.0	1763	4	US-09-244-805-57	Sequence 57, Appl
42	22	88.0	4909	3	US-08-556-978B-78	Sequence 78, Appl
43	22	88.0	6043	4	US-09-630-929-4	Sequence 4, Appl
44	22	88.0	7652	1	US-07-590-988A-1	Sequence 1, Appl
45	21.2	84.8	25	3	US-09-233-493-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-233-493-9
; Sequence 9, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-493-9

Query Match 90.4%; Score 22.6; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.96;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAASAKGW 25
|||||:||||:||||:||||:||||:|
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 2
US-09-233-493-10
; Sequence 10, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-233-493-10

Query Match 90.4%; Score 22.6; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.96;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAASAKGW 25
|||||:||||:||||:||||:||||:|
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 3
US-09-005-476-9
; Sequence 9, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:

; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-005-476-9

Query Match 90.4%; Score 22.6; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.96;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAASAKGW 25
|||||:||||:||||:||||:||||:|
Db 1 GTTCAGCTTTTGTACAAACTTGT 25

RESULT 4
US-09-005-476-10
; Sequence 10, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,476
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002

;; FILING DATE: 07-JUN-1996
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 25 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; MOLECULE TYPE: cdna
US-09-005-476-10

Query Match 90.4%; Score 22.6; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.96;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAASTKGW 25
Db 1 GTTCAGCTTTTCTGTACAACTTGT 25

RESULT 5
US-09-233-492-9
; Sequence 9, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-492-9

Query Match 90.4%; Score 22.6; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.96;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAASTKGW 25
Db 1 GTTCAGCTTTTCTGTACAACTTGT 25

RESULT 6
US-09-233-492-10
; Sequence 10, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-492-9

Query Match 90.4%; Score 22.6; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.96;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAASTKGW 25

Db 1 GTTCAGCTTTTCTGTACAACTTGT 25

RESULT 6
US-09-233-492-10
; Sequence 10, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,492
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-492-10

Query Match 90.4%; Score 22.6; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.96;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAASTKGW 25
Db 1 GTTCAGCTTTTCTGTACAACTTGT 25

RESULT 7
US-09-296-280-9
; Sequence 9, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-492-10

Query Match 90.4%; Score 22.6; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.96;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAASTKGW 25
Db 1 GTTCAGCTTTTCTGTACAACTTGT 25

RESULT 7
US-09-296-280-9
; Sequence 9, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
US-09-233-492-10

Query Match 90.4%; Score 22.6; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.96;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAASTKGW 25
Db 1 GTTCAGCTTTTCTGTACAACTTGT 25

RESULT 7
US-09-296-280-9
; Sequence 9, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22

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; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-9

Query Match          90.4%; Score 22.6; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.96;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAASTKGW 25
   |||||:||||:||||:||||:||||:|
Db 1 GTTCAGCTTTTGTGACAACTTGT 25

RESULT 8
US-09-296-280-10
; Sequence 10, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-10

Query Match          90.4%; Score 22.6; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.96;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAASTKGW 25
   |||||:||||:||||:||||:||||:|
Db 1 GTTCAGCTTCTGTGACAACTTGT 25

RESULT 9
US-09-296-280-11
; Sequence 11, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-11

Query Match          90.4%; Score 22.6; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.96;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAASTKGW 25
   |||||:||||:||||:||||:||||:|
Db 1 GTTCAGCTTCTGTGACAACTTGT 25

RESULT 10
US-09-296-280-42
; Sequence 42, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-42

Query Match          90.4%; Score 22.6; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAASTKGW 25
   |||||:||||:||||:||||:||||:|
Db 1 GTTCAGCTTTTTRTACWAASTKGW 25

RESULT 11
US-09-498-074-9
; Sequence 9, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
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; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-11

Query Match          90.4%; Score 22.6; DB 3; Length 25;
Best Local Similarity 76.0%; Pred. No. 0.96;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTTCAGCTTTTCTGTACAAAGTGT 25

RESULT 10
US-09-296-280-42
; Sequence 42, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-42

Query Match          90.4%; Score 22.6; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAASTKGW 25
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Db 1 GTTCAGCTTTTTRTACWAASTKGW 25

RESULT 11
US-09-498-074-9
; Sequence 9, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:34:49 ; Search time 314 Seconds

(without alignments)
430.015 Million cell updates/sec

Title: US-10-820-133-42

Perfect score: 25

Sequence: 1 gttcagctttttrttacwaastkgw 25

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	22.6	90.4	25	9	US-09-855-797A-9
4	22.6	90.4	25	9	US-09-855-797A-10
5	22.6	90.4	25	9	US-09-855-797A-11
6	22.6	90.4	25	9	US-09-855-797A-42
7	22.6	90.4	25	9	US-09-907-900-9
8	22.6	90.4	25	9	US-09-907-900-10
9	22.6	90.4	25	9	US-09-907-900-11
10	22.6	90.4	25	9	US-09-907-900-42
11	22.6	90.4	25	9	US-09-907-719-9
12	22.6	90.4	25	9	US-09-907-719-10

13	22.6	90.4	25	9	US-09-907-719-11
14	22.6	90.4	25	9	US-09-907-719-42
15	22.6	90.4	25	10	US-09-432-085-9
16	22.6	90.4	25	10	US-09-432-085-10
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18	22.6	90.4	25	10	US-09-985-448-10
19	22.6	90.4	25	10	US-09-985-448-11
20	22.6	90.4	25	10	US-09-985-448-42
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30	22.6	90.4	25	15	US-10-161-403-50
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34	22.6	90.4	25	15	US-10-300-892-10
35	22.6	90.4	25	15	US-10-300-892-11
36	22.6	90.4	25	15	US-10-300-892-42
37	22.6	90.4	25	16	US-10-301-849A-26
38	22.6	90.4	25	16	US-10-301-849A-30
39	22.6	90.4	25	16	US-10-680-316-9
40	22.6	90.4	25	16	US-10-680-316-10
41	22.6	90.4	25	16	US-10-680-316-11
42	22.6	90.4	25	16	US-10-680-316-42
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44	22.6	90.4	25	17	US-10-815-730-10
45	22.6	90.4	25	17	US-10-815-730-11

ALIGNMENTS

RESULT 1

US-09-732-914-8
; Sequence 8, Application US/09732914
; Patent No. US20020007051A1

; GENERAL INFORMATION:
; APPLICANT: Chco, David

; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.

; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.

; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in
; FILE REFERENCE: 0942.5010002
; CURRENT APPLICATION NUMBER: US/09/732,914

; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,983

; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/188,020

; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 140

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8

; LENGTH: 25

; TYPE: DNA

; ORGANISM: attr1

US-09-732-914-8

Query Match 90.4%; Score 22.6; DB 9; Length 25;

Best Local Similarity 76.0%; Pred. No. 2.9;

Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTTRTTACWAASTKGW 25

DB 1 GTTCAGCTTTTGTGACAACTTGT 25

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RESULT 2
US-09-732-914-12
; Sequence 12, Application US/09732914
; Patent No. US2002007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Hartley, James L.
; APPLICANT: Byrd, Devon R.N.
; TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in
; TITLE OF INVENTION: Recombinational Cloning
; FILE REFERENCE: 0942.5010002
; CURRENT APPLICATION NUMBER: US/09/732,914
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 25
; TYPE: DNA
; ORGANISM: attr2
US-09-732-914-12

Query Match          90.4%; Score 22.6; DB 9; Length 25;
Best Local Similarity 76.0%; Pred. No. 2.9;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GTTCAGCTTTCTTGACAAAGTGT 25

RESULT 3
US-09-855-797A-9
; Sequence 9, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
US-09-855-797A-9

Query Match          90.4%; Score 22.6; DB 9; Length 25;
Best Local Similarity 76.0%; Pred. No. 2.9;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GTTCAGCTTTTCTTGACAAAGTGT 25

RESULT 4
US-09-855-797A-10
; Sequence 10, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
US-09-855-797A-10

Query Match          90.4%; Score 22.6; DB 9; Length 25;
Best Local Similarity 76.0%; Pred. No. 2.9;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GTTCAGCTTTCTTGACAAACTGT 25

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US-09-855-797A-11
; Sequence 11, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
US-09-855-797A-11

Query Match          90.4%; Score 22.6; DB 9; Length 25;
Best Local Similarity 76.0%; Pred. No. 2.9;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4
US-09-855-797A-10
; Sequence 10, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
US-09-855-797A-10

Query Match          90.4%; Score 22.6; DB 9; Length 25;
Best Local Similarity 76.0%; Pred. No. 2.9;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTTRTACWAASTKGW 25
|||||:||||:||||:||||:||||:
DB 1 GTTCAGCTTTCTTGACAAACTGT 25

RESULT 5
US-09-855-797A-11
; Sequence 11, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
US-09-855-797A-11

Query Match          90.4%; Score 22.6; DB 9; Length 25;
Best Local Similarity 76.0%; Pred. No. 2.9;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
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Matches 19: Conservative 6: Mismatches 0: Indels 0: Gaps 0:

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Dd

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RESULT 10
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; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-42

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RESULT 11
US-09-907-719-9
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; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-719-9

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Db
1 GTTCAGCTTTTGTACAAACTGT 25

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RESULT 12
US-09-907-719-10
; Sequence 10, Application US/09907719
; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Braach, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-719-10

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RESULT 13
US-09-907-719-11
; Sequence 11, Application US/09907719
; Publication NO. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
; US-09-907-719-11

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US-09-907-119-9
Query Match          90.4%; Score 22.6; DB 9; Length 25;
Best Local Similarity 76.0%; Pred. No. 2.9;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
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Query Match          90.4%; Score 22.6; DB 9; Length 25;
Best Local Similarity 76.0%; Pred.No.2.9;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0
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Db      1 GTTCAGCTTTCTGTACAAAGTGGT 25

RESULT 14
US-09-907-719-42
; Sequence 42, Application US/09907719
; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 42
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-719-42

Query Match      90.4%; Score 22.6; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. NO. 2.9;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTTCAGCTTTTTRTACWAASTKGW 25
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Db      1 GTTCAGCTTTTTRTACWAASTKGW 25

RESULT 15
US-09-432-085-9
; Sequence 9, Application US/09432085
; Publication No. US20030100110A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
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; FILING DATE: 07-JUN-1996
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; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-432-085-9

Query Match      90.4%; Score 22.6; DB 10; Length 25;
Best Local Similarity 76.0%; Pred. NO. 2.9;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTTCAGCTTTTTRTACWAASTKGW 25
|||||
Db      1 GTTCAGCTTTTGTACAAACTTGT 25

Search completed: November 16, 2004, 11:15:01
Job time : 315.1 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:04 ; Search time 1532 Seconds
(without alignments)
594.643 Million cell updates/sec

Title: US-10-820-133-42
Perfect score: 25
Sequence: 1 gttcagctttttttacwaaastkgw 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsel:*
9: gb_gsel2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	22.6	90.4	708	8 AQ990869	AQ990869 Rfc01706
C 2	22.6	90.4	770	8 AQ991774	AQ991774 Rfc02039F
C 3	22.6	90.4	791	8 AQ991791	AQ991791 Rfc02368F
C 4	22	88.0	206	5 BQ156416	BQ156416 NF092F021
C 5	22	88.0	299	5 BV115594	BV115594 BV115594
C 6	22	88.0	306	5 BP757615	BP757615 BP757615
C 7	22	88.0	374	5 BP754432	BP754432 BP754432
C 8	22	88.0	401	5 BP754410	BP754410 BP754410
C 9	22	88.0	409	5 BP754552	BP754552 BP754552
C 10	22	88.0	422	5 BP754464	BP754464 BP754464
C 11	22	88.0	423	5 BP754551	BP754551 BP754551
C 12	22	88.0	430	5 BP754589	BP754589 BP754589
C 13	22	88.0	432	5 BP754563	BP754563 BP754563
C 14	22	88.0	443	5 BP754508	BP754508 BP754508
C 15	22	88.0	443	5 BP754571	BP754571 BP754571
C 16	22	88.0	449	5 BP754440	BP754440 BP754440
C 17	22	88.0	472	5 BQ157398	BQ157398 NF104D071
C 18	22	88.0	473	5 BQ156404	BQ156404 NF032E031
C 19	22	88.0	482	5 BP754592	BP754592 BP754592
C 20	22	88.0	483	5 BP757892	BP757892 BP757892
C 21	22	88.0	486	5 BP754503	BP754503 BP754503
C 22	22	88.0	489	5 BP754581	BP754581 BP754581
C 23	22	88.0	546	5 BP754439	BP754439 BP754439
C 24	22	88.0	567	5 BP754491	BP754491 BP754491

C 25	22	88.0	597	4 BI422679	BI422679 EST513345
C 26	22	88.0	645	5 BP754484	BP754484 BP754484
C 27	22	88.0	671	5 BP754388	BP754388 BP754388
C 28	22	88.0	672	5 BP754535	BP754535 BP754535
C 29	22	88.0	672	8 AQ990864	AQ990864 Rfc01701
C 30	22	88.0	674	5 BP754519	BP754519 BP754519
C 31	22	88.0	689	5 BP754572	BP754572 BP754572
C 32	22	88.0	695	8 AQ991039	AQ991039 Rfc01894
C 33	22	88.0	712	8 AQ990809	AQ990809 Rfc01638
C 34	22	88.0	731	5 BP758121	BP758121 BP758121
C 35	22	88.0	743	8 AQ990346	AQ990346 Rfc01106
C 36	22	88.0	753	8 AQ990861	AQ990861 Rfc01698
C 37	22	88.0	764	8 AQ990110	AQ990110 Rfc00827
C 38	22	88.0	769	8 AQ990470	AQ990470 Rfc01245
C 39	22	88.0	808	8 AQ990388	AQ990388 Rfc01153
C 40	21.6	86.4	756	8 AQ991732	AQ991732 Rfc00380F
C 41	21.4	85.6	821	9 CL672759	CL672759 PRI017d A
C 42	21.4	85.6	875	9 CL688994	CL688994 PRI0150a
C 43	21	84.0	395	8 AQ991303	AQ991303 Rfc02205-
C 44	21	84.0	664	8 AQ991011	AQ991011 Rfc01864
C 45	21	84.0	719	8 AQ991352	AQ991352 Rfc02270

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
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Rfc01706 Photorhabdus luminescens strain W14 M13 library
Photobacterium luminescens genomic clone PLG01706, genomic survey
sequence.
ACCESSION
AQ990869
VERSION
AQ990869.1
KEYWORDS
GSS.
SOURCE
Photobacterium luminescens
ORGANISM
Photobacterium luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE
1 (bases 1 to 708)
ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photobacterium luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
20378633
10919786
Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsarfbath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.
Location/Qualifiers
1. .708
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/clone="PLG01706"
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/clone_lib="Photobacterium luminescens strain W14 M13
library"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

ORIGIN

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 Best Local Similarity 76.0%; Pred. No. 43;
 Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAASTKGM 25
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 Db 348 GTTCAGCTTTTATACTACTGGA 324

RESULT 2
 AQ991774/c
 LOCUS
 DEFINITION Rfc02039F Photorhabdus luminescens strain W14 M13 library GSS 14-AUG-2000
 Photorhabdus luminescens genomic clone PLG02039F, genomic survey sequence.

ACCESSION AQ991774
 VERSION AQ991774.1 GI:9650368
 KEYWORDS GSS.

SOURCE
 ORGANISM Photorhabdus luminescens
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Photorhabdus.

REFERENCE
 AUTHORS 1 (bases 1 to 770)
 fFrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
 Daborn,P.J., Bowen,D. and Blattner,F.R.

TITLE
 A genomic sample sequence of the entomopathogenic bacterium
 Photorhabdus luminescens W14: potential implications for virulence

JOURNAL
 MEDLINE Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
 PUBMED 20378633

COMMENT
 Contact: fFrench-Constant 'RH
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 University of Bath

South Building, Bath BA2 7AY, UK
 Tel: (44) 1225 826621
 Fax: (44) 1225 826779

Email: bssrfc@bath.ac.uk
 This is one of a selected subset of flipped clones from the M13
 library. For annotation of identified clones (BLASTX, BLASTN and
 mapping to E. coli K12 genome) please see fFrench-Constant et al.
 2000, Nucleic Acids Res.

Seq primer: M13 Reverse
 Class: shotgun.

FEATURES
 source
 Location/Qualifiers
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/organism="Photorhabdus luminescens"
 /mol_type="genomic DNA"
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 /note="Genomic DNA from strain W14 was size selected (1-2
 kb) and then cloned into M13 Janus."

ORIGIN

Query Match 90.4%; Score 22.6; DB 8; Length 770;
 Best Local Similarity 76.0%; Pred. No. 44;
 Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAASTKGM 25
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 Db 59 GTTCAGCTTTTATACTACTGGA 35

RESULT 3
 AQ991791/c
 LOCUS
 DEFINITION Rfc02368F Photorhabdus luminescens strain W14 M13 library GSS 14-AUG-2000
 Photorhabdus luminescens genomic clone PLG02368F, genomic survey sequence.

ACCESSION AQ991791
 VERSION AQ991791.1 GI:9650385
 KEYWORDS GSS.

SOURCE
 ORGANISM Photorhabdus luminescens

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Photorhabdus.

REFERENCE
 AUTHORS 1 (bases 1 to 791)

fFrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
 Daborn,P.J., Bowen,D. and Blattner,F.R.

A genomic sample sequence of the entomopathogenic bacterium
 Photorhabdus luminescens W14: potential implications for virulence
 Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

JOURNAL
 MEDLINE 20378633
 PUBMED 10919786

COMMENT
 Contact: fFrench-Constant RH
 Department of Biology and Biochemistry
 University of Bath

South Building, Bath BA2 7AY, UK
 Tel: (44) 1225 826621
 Fax: (44) 1225 826779

Email: bssrfc@bath.ac.uk
 This is one of a selected subset of flipped clones from the M13
 library. For annotation of identified clones (BLASTX, BLASTN and
 mapping to E. coli K12 genome) please see fFrench-Constant et al.
 2000, Nucleic Acids Res.

Seq primer: M13 Reverse
 Class: shotgun.

FEATURES
 source
 Location/Qualifiers
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 kb) and then cloned into M13 Janus."

ORIGIN

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 Best Local Similarity 76.0%; Pred. No. 44;
 Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAASTKGM 25
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 Db 56 GTTCAGCTTTTATACTACTGGA 32

RESULT 4

BQ156416/c

LOCUS

DEFINITION NF092F02IR1F1027 Irradiated Medicago truncatula cDNA clone
 NF092F02IR 5', mRNA sequence.

ACCESSION BQ156416
 VERSION BQ156416

KEYWORDS EST.
 SOURCE Medicago truncatula (barrel medic)

ORGANISM

Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 206)

Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,

Flores,H.R., Inman,J.I., Weller,J.W. and May,G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation

Medicago truncatula irradiated library

Unpublished (2001)

Contact: May GD

Plant Biology Division

The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 224 6650
Fax: 580 224 6692
Email: gdmay@noble.org
Insert Length: 206 Std Error: 0.00
Plate: 092 Row: F Column: 02
Seq primer: TCACACAGAAACACTGAC.
Location/Qualifiers
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FEATURES

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ORIGIN

Query Match 88.0%; Score 22; DB 5; Length 206;
Best Local Similarity 79.2%; Pred No. 68;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAATKG 24

Db 167 GTTCAGCTTTTATCTAAGTTG 144

RESULT 5
BY115594
LOCUS
DEFINITION
musculus cDNA clone L430040C03 5', mRNA sequence.
EST.
BY115594.1 GI:26226695
Mus musculus (house mouse)
ORGANISM

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 209)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bratt, D., Brusci, V., Chotha, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konggay, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramchandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,

Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Haseizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

TITLE

JOURNAL
MEDLINE
PUBMED
COMMENT

Nature 420, 563-573 (2002)

22354583

12466851

Contact: Yoshihide Hayashizaki

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The Institute of Physical and Chemical Research (RIKEN)

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Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/

Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,

Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,

Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,

Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,

Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and

Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Please visit our web site (http://genome.gsc.riken.go.jp) for

further details.

FEATURES
source

Location/Qualifiers

1..293

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/clone="L430040C03"

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whole body"

ORIGIN

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Best Local Similarity 79.2%; Pred. No. 71;

Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAATKG 24

Db 246 GTTCAGCTTTTATCTAAGTTG 269

RESULT 6

BP757615/c

LOCUS

BP757615 mouse (C57BL/6) pancreatic islet library with

recombination-based method Mus musculus cDNA clone mib04031 3',

306 bp mRNA linear

EST 08-JUL-2004

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mRNA sequence.
ACCESSION BP757615
VERSION BP757615.1 GI:50077505
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
Takeda,J., Ohara,O. and Seino,S.
TITLE Construction of a multi-functional cDNA library specific for mouse
pancreatic islets and its application to microarray
JOURNAL Unpublished (2004)
COMMENT Contact: Susumu Seino
Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.

FEATURES
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ORIGIN
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Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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DB 109 GTTCAGCTTTTGTACAAAGTTG 86

RESULT 7
BP754432/c
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DEFINITION BP754432 mouse (C57BL/6) pancreatic islet library with
recombination-based method Mus musculus cDNA clone mial0061 3',
mRNA sequence.
ACCESSION BP754432
VERSION BP754432.1 GI:50074322
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
Takeda,J., Ohara,O. and Seino,S.
TITLE Construction of a multi-functional cDNA library specific for mouse
pancreatic islets and its application to microarray
JOURNAL Unpublished (2004)
COMMENT Contact: Susumu Seino
Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.

FEATURES
source
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recombination-based method"

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Best Local Similarity 79.2%; Pred. No. 73;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCAGCTTTTTRTACWAASTKG 24
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DB 73 GTTCAGCTTTTGTACAAAGTTG 50

RESULT 8
BP754410/c
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DEFINITION BP754410 mouse (C57BL/6) pancreatic islet library with
recombination-based method Mus musculus cDNA clone mial0045 3',
mRNA sequence.
ACCESSION BP754410
VERSION BP754410.1 GI:50074300
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
Takeda,J., Ohara,O. and Seino,S.
TITLE Construction of a multi-functional cDNA library specific for mouse
pancreatic islets and its application to microarray
JOURNAL Unpublished (2004)
COMMENT Contact: Susumu Seino
Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.

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DEFINITION BP754552 mouse (C57BL/6) pancreatic islet library with

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recombination-based method Mus musculus cDNA clone mial1051 3',
mRNA sequence.
ACCESSION BP754552
VERSION BP754552.1 GI:50074442
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 409)
AUTHORS Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
Takeda,J., Ohara,O. and Seino,S.
TITLE Construction of a multi-functional cDNA library specific for mouse
pancreatic islets and its application to microarray
JOURNAL
COMMENT Unpublished (2004)
Contact: Susumu Seino
Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.
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mRNA sequence.
ACCESSION BP754464
VERSION BP754464.1 GI:50074354
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 422)
AUTHORS Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
Takeda,J., Ohara,O. and Seino,S.
TITLE Construction of a multi-functional cDNA library specific for mouse
pancreatic islets and its application to microarray
JOURNAL
COMMENT Unpublished (2004)
Contact: Susumu Seino
Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.
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Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
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mRNA sequence.
ACCESSION BP754551
VERSION BP754551.1 GI:50074441
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 423)
AUTHORS Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
Takeda,J., Ohara,O. and Seino,S.
TITLE Construction of a multi-functional cDNA library specific for mouse
pancreatic islets and its application to microarray
JOURNAL
COMMENT Unpublished (2004)
Contact: Susumu Seino
Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.
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DEFINITION BP754571 mouse (C57BL/6) pancreatic islet library with
recombination-based method Mus musculus cDNA clone mial1066 3',
mRNA sequence.
ACCESSION BP754571
VERSION BP754571.1 GI:50074461
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 443)
AUTHORS Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
Takeda,J., Ohara,O. and Seino,S.
TITLE Construction of a multi-functional cDNA library specific for mouse
pancreatic islets and its application to microarray
JOURNAL Unpublished (2004)
COMMENT Contact: Susumu Seino
Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-Ku, Kobe, Hyogo 650-0017, Japan
Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.
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6	23.8	95.2	25	6	AR163187	Sequence
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11	23.8	95.2	25	6	AX491650	Sequence
12	23.8	95.2	25	6	AX491654	Sequence
13	23.8	95.2	25	6	AX491655	Sequence
14	23.8	95.2	25	6	AX498621	Sequence
15	23.8	95.2	25	6	AX498625	Sequence
16	23.8	95.2	25	6	AX498626	Sequence
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ACCESSION AR124536
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KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
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Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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LOCUS
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ACCESSION AR163182
VERSION AR163182.1 GI:162233692
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6270969-A 11 07-AUG-2001;
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DEFINITION Sequence 11 from patent US 6270969.
ACCESSION AR163182
VERSION AR163182.1 GI:162233692
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REFERENCE
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6270969-A 11 07-AUG-2001;
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REFERENCE
AUTHORS Hartley, J.L. and Brasch, M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1227147-A 15 31-JUL-2002;
INVITROGEN CORPORATION (US)
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ACCESSION AX498625
VERSION AX498625.1 GI:23343422
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REFERENCE 1
AUTHORS Hartley, J.L. and Brasch, M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1229113-A 15 07-AUG-2002;
INVITROGEN CORPORATION (US)
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Job time : 709.5 secs

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AUTHORS Hartley, J.L. and Brasch, M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1227147-A 15 31-JUL-2002;
INVITROGEN CORPORATION (US)
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ACCESSION AX491655
VERSION AX491655.1 GI:22324163
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Hartley, J.L. and Brasch, M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1227147-A 16 31-JUL-2002;
INVITROGEN CORPORATION (US)
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DEFINITION Sequence 11 from Patent EP1229113.
ACCESSION AX498621
VERSION AX498621.1 GI:23343418
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Hartley, J.L. and Brasch, M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1229113-A 11 07-AUG-2002;
INVITROGEN CORPORATION (US)
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GenCore version 5.1.1.6
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Run on: November 16, 2004, 03:29:13 ; Search time 167.8 Seconds
(without alignments)
782.095 Million cell updates/sec

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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26	23.8	95.2	25	9	ACD28486	AcD28486 Nucleic a
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ALIGNMENTS

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KW vector; subcloning; regulation; exchange; ss.
OS Synthetic.
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PN WO9640724-A1.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US010082.
XX
PR 07-JUN-1995; 95US-00486139.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX Hartley JL, Brasch MA;
XX WPI; 1997-065168/06.
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XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
XX using recombinant proteins and engineered recombination sites in vitro or
XX in vivo.
XX
XX Claim 14; Page 56; 106pp; English.
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XX AAT48210-25 are att recombination site core region DNA sequences. The
XX core region has at least one engineered mutation that enhances
XX recombination in vitro in the formation of a Cointegrate or Product DNA.
XX These core regions can be incorporated into novel vector donor DNA
XX molecules. The nucleic acids, vectors and methods of the invention are
XX used to obtain chimeric nucleic acid using recombination proteins and
XX engineered recombination sites in vitro or in vivo. The improved
XX specificity, speed and yields of the invention facilitates DNA or RNA
XX subcloning, regulation or exchange useful for any related purpose, e.g.

OS Synthetic.
 XX WO9921977-A1.
 PN
 XX
 PD 06-MAY-1999.
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 PF 26-OCT-1998; 98WO-US022589.
 XX
 XX 24-OCT-1997; 97US-0065930P.
 PR 23-OCT-1998; 98US-00177387.
 XX
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hartley JL, Brasch MA, Temple GF, Fox DK;
 XX WPI; 1999-303011/25.
 DR
 XX New nucleic acid cloning methods.
 XX
 XX Disclosure; Page 163; 185pp; English.
 XX
 CC The invention relates to novel methods for cloning or subcloning one or
 CC more nucleic acid molecules (NAMEs) comprising: (a) combining in vitro or
 CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
 CC more desired nucleic acid segments flanked by at least 2 recombination
 CC sites which do not recombine with each other; (2) one or more vector
 CC donor molecules (VDMs) comprising at least 2 recombination sites which do
 CC not recombine with each other; and (3) one or more site-specific
 CC recombination proteins; (b) incubating the combination to transfer one or
 CC more of the desired segments into one or more of the VDMs, thereby
 CC producing one or more desired product molecules (PMs). The methods can be
 CC used for the efficient and specific recombination of NAME segments. They
 CC can be used to generate chimeric DNA or RNA molecules that have the
 CC desired characteristics and/or nucleic acid segments. The methods can
 CC also be used for changing vectors. The oligonucleotides AAX78935-X78994
 CC are used in the method of the invention
 XX
 SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 U; 0 Other;
 Query Match 95.2%; Score 23.8; DB 2; Length 25;
 Best Local Similarity 88.0%; Pred. No. 1.6;
 Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GTTCAGCTTTTCTTACWAAGTTGG 25
 Db 1 GTTCAGCTTTTCTTACWAAGTTGG 25
 RESULT 5
 AAX78949
 ID AAX78949 standard; DNA; 25 BP.
 AC
 XX
 AC AAX78949;
 XX
 DT 17-AUG-1999 (first entry)
 XX
 DE Oligonucleotide #15 for recombination and cloning method.
 XX
 XX Cloning; donor; recombination site; vector; chimeric; ss.
 KW
 XX Synthetic.
 OS
 XX WO9921977-A1.
 PN
 XX
 PD 06-MAY-1999.
 XX
 XX 26-OCT-1998; 98WO-US022589.
 PF
 XX 24-OCT-1997; 97US-0065930P.
 PR 23-OCT-1998; 98US-00177387.
 XX
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PA
 XX

PI Hartley JL, Brasch MA, Temple GF, Fox DK;
 XX WPI; 1999-303011/25.
 DR
 XX New nucleic acid cloning methods.
 XX
 XX Disclosure; Page 162; 185pp; English.
 XX
 CC The invention relates to novel methods for cloning or subcloning one or
 CC more nucleic acid molecules (NAMEs) comprising: (a) combining in vitro or
 CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
 CC more desired nucleic acid segments flanked by at least 2 recombination
 CC sites which do not recombine with each other; (2) one or more vector
 CC donor molecules (VDMs) comprising at least 2 recombination sites which do
 CC not recombine with each other; and (3) one or more site-specific
 CC recombination proteins; (b) incubating the combination to transfer one or
 CC more of the desired segments into one or more of the VDMs, thereby
 CC producing one or more desired product molecules (PMs). The methods can be
 CC used for the efficient and specific recombination of NAME segments. They
 CC can be used to generate chimeric DNA or RNA molecules that have the
 CC desired characteristics and/or nucleic acid segments. The methods can
 CC also be used for changing vectors. The oligonucleotides AAX78935-X78994
 CC are used in the method of the invention
 XX
 SQ Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 U; 0 Other;
 Query Match 95.2%; Score 23.8; DB 2; Length 25;
 Best Local Similarity 88.0%; Pred. No. 1.6;
 Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GTTCAGCTTTTCTTACWAAGTTGG 25
 Db 1 GTTCAGCTTTTCTTACWAAGTTGG 25
 RESULT 6
 AAC87880
 ID AAC87880 standard; DNA; 25 BP.
 AC
 XX
 AC AAC87880;
 XX
 DT 02-MAR-2001 (first entry)
 XX
 DE Escherichia coli core region recombinant site attP1 SEQ ID NO:15.
 XX
 XX Core region; recombination site; cloning; chimeric DNA; characteristic;
 KW mutation; att site; lox site; ss.
 XX
 OS Escherichia coli.
 XX
 XX US6143557-A.
 PN
 XX
 PD 07-NOV-2000.
 XX
 PF 20-JAN-1999; 99US-00233493.
 XX
 XX 07-JUN-1995; 95US-00486139.
 PR 07-JUN-1996; 96US-00663002.
 XX
 XX 12-JAN-1998; 98US-00005476.
 XX
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 PA
 XX Brasch MA, Hartley JL;
 PI
 XX WPI; 2001-049004/06.
 DR
 XX Isolated nucleic acid molecules comprising a DNA segment having two
 XX engineered recombination sites, derived from att or lox, which flank a
 XX selectable marker and comprise a core region having an engineered
 XX mutation.
 XX
 XX Claim 1; Col 18; 73pp; English.
 PS
 XX

CC The present invention describes an isolated nucleic acid molecule (I)
 CC comprising a first nucleic acid sequence having a defined sequence
 CC (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,
 CC or an RNA sequence corresponding to AAC87866 to AAC87881. Also described
 CC are: (1) an isolated nucleic acid molecule (II) comprising a first
 CC mutated recombination site that removes one or more stop codons from the
 CC recombination site or avoids hairpin formation, the recombination site
 CC being an att or lox site; (2) an isolated nucleic acid molecule (III)
 CC comprising a first att recombination site comprising a mutation that
 CC enhances recombination specificity; (3) vectors (IV) comprising the above
 CC mentioned nucleic acids; and (4) cells comprising the above mentioned
 CC nucleic acids or (IV). The nucleic acids are used in engineering a core
 CC region of a given recombination site to provide mutative sites suitable
 CC for subcloning reactions. The use of nucleic acids for obtaining
 CC engineered recombination in vitro or in vivo makes the methods for DNA or
 CC RNA subcloning, highly specific, rapid, and less labour intensive
 XX

SQ Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 U; 0 Other;

Query Match 95.2%; Score 23.8; DB 4; Length 25;
 Best Local Similarity 88.0%; Pred. No. 1.6;
 Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTCTTACAAAGTTGG 25
 |||||:||||:||||:
 Db 1 GTTCAGCTTTTCTTACAAAGTTGG 25

RESULT 7

AAC87876

ID AAC87876 standard; DNA; 25 BP.

XX AAC87876;

XX 02-MAR-2001 (first entry)

XX Escherichia coli core region recombinant site attr3 SEQ ID NO:11.

XX Core region; recombination site; cloning; chimeric DNA; characteristic;
 KW mutation; att site; lox site; ss.

XX Escherichia coli.

XX US6143557-A.

XX 07-NOV-2000.

XX 20-JAN-1999; 99US-00233493.

XX 07-JUN-1995; 95US-00486139.

XX 07-JUN-1996; 96US-00663002.

XX 12-JAN-1998; 98US-00005476.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Brasch MA, Hartley JL;

XX WPI; 2001-049004/06.

XX Isolated nucleic acid molecules comprising a DNA segment having two
 PT engineered recombination sites, derived from att or lox, which flank a
 PT selectable marker and comprise a core region having an engineered
 PT mutation.

XX Claim 1; Col 18; 73pp; English.

XX The present invention describes an isolated nucleic acid molecule (I)
 CC comprising a first nucleic acid sequence having a defined sequence
 CC (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,
 CC or an RNA sequence corresponding to AAC87866 to AAC87881. Also described
 CC are: (1) an isolated nucleic acid molecule (II) comprising a first
 CC mutated recombination site that removes one or more stop codons from the
 CC recombination site or avoids hairpin formation, the recombination site

CC being an att or lox site; (2) an isolated nucleic acid molecule (III)
 CC comprising a first att recombination site comprising a mutation that
 CC enhances recombination specificity; (3) vectors (IV) comprising the above
 CC mentioned nucleic acids; and (4) cells comprising the above mentioned
 CC nucleic acids or (IV). The nucleic acids are used in engineering a core
 CC region of a given recombination site to provide mutative sites suitable
 CC for subcloning reactions. The use of nucleic acids for obtaining
 CC engineered recombination in vitro or in vivo makes the methods for DNA or
 CC RNA subcloning, highly specific, rapid, and less labour intensive
 XX

SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 U; 0 Other;

Query Match 95.2%; Score 23.8; DB 4; Length 25;

Best Local Similarity 88.0%; Pred. No. 1.6;

Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTCTTACAAAGTTGG 25
 |||||:||||:||||:
 Db 1 GTTCAGCTTTTCTTACAAAGTTGG 25

RESULT 8

AAC87881

ID AAC87881 standard; DNA; 25 BP.

XX AAC87881;

XX 02-MAR-2001 (first entry)

XX Escherichia coli core region recombinant site attP2,P3 SEQ ID NO:16.

XX Core region; recombination site; cloning; chimeric DNA; characteristic;
 KW mutation; att site; lox site; ss.

XX Escherichia coli.

XX US6143557-A.

XX 07-NOV-2000.

XX 20-JAN-1999; 99US-00233493.

XX 07-JUN-1995; 95US-00486139.

XX 07-JUN-1996; 96US-00663002.

XX 12-JAN-1998; 98US-00005476.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Brasch MA, Hartley JL;

XX WPI; 2001-049004/06.

XX Isolated nucleic acid molecules comprising a DNA segment having two
 PT engineered recombination sites, derived from att or lox, which flank a
 PT selectable marker and comprise a core region having an engineered
 PT mutation.

XX Claim 1; Col 18; 73pp; English.

XX The present invention describes an isolated nucleic acid molecule (I)
 CC comprising a first nucleic acid sequence having a defined sequence
 CC (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881,
 CC or an RNA sequence corresponding to AAC87866 to AAC87881. Also described
 CC are: (1) an isolated nucleic acid molecule (II) comprising a first
 CC mutated recombination site that removes one or more stop codons from the
 CC recombination site or avoids hairpin formation, the recombination site
 CC being an att or lox site; (2) an isolated nucleic acid molecule (III)
 CC comprising a first att recombination site comprising a mutation that
 CC enhances recombination specificity; (3) vectors (IV) comprising the above
 CC mentioned nucleic acids; and (4) cells comprising the above mentioned
 CC nucleic acids or (IV). The nucleic acids are used in engineering a core
 CC region of a given recombination site to provide mutative sites suitable
 CC for subcloning reactions. The use of nucleic acids for obtaining


```

PN US6171861-B1.
XX
XX
PD 09-JAN-2001.
XX
XX 12-JAN-1998; 99US-00005476.
XX
XX 07-JUN-1995; 95US-00486139.
XX
XX 07-JUN-1996; 96US-00663002.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Hartley JL, Brasch MA;
XX
XX WPI; 2001-136877/14.
XX
XX In vitro cloning of nucleic acid involves mixing vectors comprising
PT recombination sites and/or nucleic acid, incubating mixture to produce
PT chimeric molecule, contacting hosts with mixture and selecting host.
XX
XX Claim 25; Col 46; 73pp; English.
XX
XX The present invention relates to a method for in vitro cloning of a
CC nucleic acid of interest. The method involves mixing in vitro two vectors
CC each comprising at least one recombination site and the nucleic acid of
CC interest; incubating the mixture in the presence of at least one
CC recombination protein to result in recombination of the recombination
CC sites, leading to production of a chimeric nucleic acid molecule
CC comprising the nucleic acid of interest; contacting hosts with the
CC mixture; and selecting for a host comprising the chimeric nucleic acid
CC molecule, and selecting against a host comprising the vectors comprising
CC the second vector, to clone the nucleic acid. The present sequence is a
CC recombination site, which may be used in the method of the present
XX invention
XX
XX Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 U; 0 Other;
SQ
Query Match 95.2%; Score 23.8; DB 4; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.6;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTTRTACWAAGTTGG 25
DB 1 GTTCAGCTTTCTGTACAAAGTTGG 25
RESULT 12
AADI4443
ID AADI4443 standard; DNA; 25 BP.
XX
XX AADI4443;
XX
XX 01-NOV-2001 (first entry)
XX
XX Recombination site attP1 DNA.
XX
XX Recombination site; copy number; replicon; recombinatorial cloning;
XX attP1; ds.
XX
XX Unidentified.
XX
XX US6270969-B1.
XX
XX 07-AUG-2001.
XX
XX 20-JAN-1999; 99US-00233492.
XX
XX 07-JUN-1995; 95US-00486139.
XX
XX 07-JUN-1996; 96US-00663002.
XX
XX (INVI-) INVITROGEN CORP.
XX
XX Hartley JL, Brasch MA;
XX
XX WPI; 2001-136877/14.
XX
XX Methods for apposing nucleic acids comprising an expression signal and a
PT gene/partial gene, using recombinatorial cloning by incubating the
PT nucleic acids in the presence of a recombination protein under conditions
PT for recombination.
XX
XX Claim 14; Col 18; 76pp; English.
XX
XX The invention relates to a method for apposing an expression signal and a
CC gene or partial gene, using recombinatorial cloning. The method incubates
CC nucleic acids comprising the expression signal and the gene/ partial gene
CC in the presence of a recombination protein under conditions sufficient to
CC cause recombination and therefore appose the expression signal and the
CC gene or partial gene. The methods are useful for apposing an expression
CC signal and a gene or partial gene using recombinatorial cloning. The
CC methods are also useful for changing vectors, constructing genes for
CC fusion proteins, changing copy number, changing replicons, cloning into
CC phages, and cloning e.g., PCR products (with an attB site at one end and
CC a loxP site at the other end), genomic DNAs, and cDNAs. The methods are
CC highly specific, rapid, and less labour intensive than prior art methods.
CC The present sequence is a recombination site useful for recombination
XX cloning
XX
XX Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 U; 0 Other;
SQ
Query Match 95.2%; Score 23.8; DB 4; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.6;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTTRTACWAAGTTGG 25
DB 1 GTTCAGCTTTTGTACAAAGTTGG 25
RESULT 13
AADI4444
ID AADI4444 standard; DNA; 25 BP.
XX
XX AADI4444;
XX
XX 01-NOV-2001 (first entry)
XX
XX Recombination site attP2,P3 DNA.
XX
XX Recombination site; copy number; replicon; recombinatorial cloning;
XX attP2,P3; ds.
XX
XX Unidentified.
XX
XX US6270969-B1.
XX
XX 07-AUG-2001.
XX
XX 20-JAN-1999; 99US-00233492.
XX
XX 07-JUN-1995; 95US-00486139.
XX
XX 07-JUN-1996; 96US-00663002.
XX
XX (INVI-) INVITROGEN CORP.
XX
XX Hartley JL, Brasch MA;
XX
XX WPI; 2001-488248/53.
XX
XX Methods for apposing nucleic acids comprising an expression signal and a
PT gene/partial gene, using recombinatorial cloning by incubating the
PT nucleic acids in the presence of a recombination protein under conditions
PT for recombination.
XX
XX Claim 14; Col 18; 76pp; English.
XX
XX The invention relates to a method for apposing an expression signal and a
XX

```


SQ Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 U; 0 Other;

Query Match 95.2%; Score 23.8; DB 5; Length 25;

Best Local Similarity 88.0%; Pred. No. 1.6;

Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAAGTTGG 25

Db 1 GTTCAGCTTTCTTGTACAAAGTTGG 25

Search completed: November 16, 2004, 04:02:50

Job time : 168.8 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:33:19 ; Search time 35.9 Seconds
(without alignments)
494.978 Million cell updates/sec

Title: US-10-820-133-43

Perfect score: 25

Sequence: 1 gttcagcttcttttacwaagtgg 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23.8	95.2	25	3	US-09-233-493-11
2	23.8	95.2	25	3	US-09-233-493-15
3	23.8	95.2	25	3	US-09-233-493-16
4	23.8	95.2	25	3	US-09-005-476-11
5	23.8	95.2	25	3	US-09-005-476-15
6	23.8	95.2	25	3	US-09-005-476-16
7	23.8	95.2	25	3	US-09-233-492-11
8	23.8	95.2	25	3	US-09-233-492-15
9	23.8	95.2	25	3	US-09-233-492-16
10	23.8	95.2	25	3	US-09-296-280-15
11	23.8	95.2	25	3	US-09-296-280-16
12	23.8	95.2	25	3	US-09-296-280-43
13	23.8	95.2	25	4	US-09-498-074-11
14	23.8	95.2	25	4	US-09-498-074-15
15	23.8	95.2	25	4	US-09-498-074-16
16	23.8	95.2	25	4	US-09-498-074-11
17	23.8	95.2	25	4	US-09-498-074-15
18	23.8	95.2	25	4	US-09-498-074-16
19	23.8	95.2	25	5	PCT-US96-10082A-11
20	23.8	95.2	25	5	PCT-US96-10082A-15
21	23.8	95.2	25	5	PCT-US96-10082A-16
22	23.8	95.2	201	1	US-08-021-667A-18
23	23.8	95.2	201	1	US-08-410-544-18
24	23.8	95.2	201	1	US-08-728-785A-18
25	23.8	95.2	1763	4	US-09-244-805-57
26	23.8	95.2	4909	3	US-08-556-978B-78
27	23.8	95.2	6043	4	US-09-630-929-4

28 23.8 95.2 7652 1 US-07-590-988A-1 Sequence 1, Appli
29 22 88.0 25 3 US-09-236-280-42 Sequence 42, Appli
30 21.2 84.8 25 3 US-09-233-493-9 Sequence 9, Appli
31 21.2 84.8 25 3 US-09-233-493-10 Sequence 10, Appli
32 21.2 84.8 25 3 US-09-005-476-9 Sequence 9, Appli
33 21.2 84.8 25 3 US-09-005-476-10 Sequence 10, Appli
34 21.2 84.8 25 3 US-09-233-492-9 Sequence 9, Appli
35 21.2 84.8 25 3 US-09-233-492-10 Sequence 10, Appli
36 21.2 84.8 25 3 US-09-236-280-9 Sequence 9, Appli
37 21.2 84.8 25 3 US-09-296-280-10 Sequence 10, Appli
38 21.2 84.8 25 3 US-09-296-280-11 Sequence 11, Appli
39 21.2 84.8 25 4 US-09-498-074-9 Sequence 9, Appli
40 21.2 84.8 25 4 US-09-498-074-10 Sequence 10, Appli
41 21.2 84.8 25 4 US-09-498-074-9 Sequence 9, Appli
42 21.2 84.8 25 4 US-09-498-074-10 Sequence 10, Appli
43 21.2 84.8 25 5 PCT-US96-10082A-9 Sequence 9, Appli
44 21.2 84.8 25 5 PCT-US96-10082A-10 Sequence 10, Appli
45 20.8 83.2 25 3 US-09-233-493-14 Sequence 14, Appli

ALIGNMENTS

RESULT 1
US-09-233-493-11
; Sequence 11, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
US-09-233-493-11

Query Match 95.2%; Score 23.8; DB 3; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.29;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAAGTTGG 25
|||||:|||||:|||||:|||||
Db 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25

RESULT 2

US-09-233-493-15
; Sequence 15, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-233-493-15

Query Match 95.2%; Score 23.8; DB 3; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.29;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAAGTTGG 25
|||||:|||||:|||||:|||||
Db 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25

RESULT 3

US-09-233-493-16
; Sequence 16, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:

; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-233-493-16

Query Match 95.2%; Score 23.8; DB 3; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.29;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAAGTTGG 25
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Db 1 GTTCAGCTTTCTTGTCACAAAGTTGG 25

RESULT 4

US-09-005-476-11
; Sequence 11, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk


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/ COUNTRY: USA
/ ZIP: 20005-3934
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/233,492
/ FILING DATE: 20-JAN-1999
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/486,139
/ FILING DATE: 07-JUN-1996
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/486,139
/ FILING DATE: 07-JUN-1996
/ CLASSIFICATION:
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: both
/ MOLECULE TYPE: cdna
US-09-233-492-11

Query Match 95.2%; Score 23.8; DB 3; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.29;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAAGTTGG 25
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Db 1 GTTCAGCTTTTCTGTACAAAGTTGG 25

RESULT 8
US-09-233-492-15
/ Sequence 15, Application US/09233492
/ Patent No. 6270969
/ GENERAL INFORMATION:
/ APPLICANT: Hartley, James L.
/ APPLICANT: Brasch, Michael A.
/ TITLE OF INVENTION: Recombinational Cloning Using Engineered
/ NUMBER OF SEQUENCES: 35
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
/ STREET: 1100 New York Ave., N. W. Suite 600
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3934
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/233,492
/ FILING DATE: 20-JAN-1999
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/663,002
/ FILING DATE: 07-JUN-1996
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/486,139
/ FILING DATE: 07-JUN-1996
/ CLASSIFICATION:
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2540
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: both
/ MOLECULE TYPE: cdna
US-09-233-492-16

Query Match 95.2%; Score 23.8; DB 3; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.29;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAAGTTGG 25
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Db 1 GTTCAGCTTTTCTGTACAAAGTTGG 25

RESULT 9
US-09-233-492-16
/ Sequence 16, Application US/09233492
/ Patent No. 6270969
/ GENERAL INFORMATION:
/ APPLICANT: Hartley, James L.
/ APPLICANT: Brasch, Michael A.
/ TITLE OF INVENTION: Recombinational Cloning Using Engineered
/ NUMBER OF SEQUENCES: 35
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
/ STREET: 1100 New York Ave., N. W. Suite 600
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3934
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/233,492
/ FILING DATE: 20-JAN-1999
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/663,002
/ FILING DATE: 07-JUN-1996
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/486,139
/ FILING DATE: 07-JUN-1996
/ CLASSIFICATION:
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2540
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: both
/ MOLECULE TYPE: cdna
US-09-233-492-16

Query Match 95.2%; Score 23.8; DB 3; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.29;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAAGTTGG 25
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Db 1 GTTCAGCTTTTCTGTACAAAGTTGG 25
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Db 1 GTTCAGCTTTCTGTGACAAAGTTGG 25
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RESULT 10
US-09-296-280-15
; Sequence 15, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; EARLIER FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-15

Query Match 95.2%; Score 23.8; DB 3; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.29;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTGTGACAAAGTTGG 25
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Db 1 GTTCAGCTTTCTGTGACAAAGTTGG 25
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RESULT 11
US-09-296-280-16
; Sequence 16, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; EARLIER FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-16

Query Match 95.2%; Score 23.8; DB 3; Length 25;
Best Local Similarity 88.0%; Pred. No. 0.29;

Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTGTGACAAAGTTGG 25
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Db 1 GTTCAGCTTTCTGTGACAAAGTTGG 25
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RESULT 12
US-09-296-280-43
; Sequence 43, Application US/09296280
; Patent No. 6277608
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850007
; CURRENT APPLICATION NUMBER: US/09/296,280
; EARLIER FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 09/177,387
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: US 60/065,930
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-296-280-43

Query Match 95.2%; Score 23.8; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTCTGTGACAAAGTTGG 25
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Db 1 GTTCAGCTTTCTGTGACAAAGTTGG 25
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RESULT 13
US-09-498-074-11
; Sequence 11, Application US/09498074
; Patent No. 6534264
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,074
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476

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Job time : 36.9 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 03:34:49 ; Search time 314 Seconds
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430.015 Million cell updates/sec

Title: US-10-820-133-43
Perfect score: 25
Sequence: 1 gtccagctttttttacwaagtgg 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

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21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	23.8	95.2	25	9	US-09-855-797A-43
4	23.8	95.2	25	9	US-09-822-634-8
5	23.8	95.2	25	9	US-09-907-900-15
6	23.8	95.2	25	9	US-09-907-900-16
7	23.8	95.2	25	9	US-09-907-900-43
8	23.8	95.2	25	9	US-09-907-719-15
9	23.8	95.2	25	9	US-09-907-719-16
10	23.8	95.2	25	9	US-09-907-719-43
11	23.8	95.2	25	10	US-09-432-085-11
12	23.8	95.2	25	10	US-09-432-085-15

13	23.8	95.2	25	10	US-09-432-085-16	Sequence 16, Appl
14	23.8	95.2	25	10	US-09-985-448-15	Sequence 15, Appl
15	23.8	95.2	25	10	US-09-985-448-16	Sequence 16, Appl
16	23.8	95.2	25	10	US-09-985-448-43	Sequence 43, Appl
17	23.8	95.2	25	14	US-10-055-001A-6	Sequence 6, Appl
18	23.8	95.2	25	14	US-10-055-001A-10	Sequence 10, Appl
19	23.8	95.2	25	14	US-10-055-001A-11	Sequence 11, Appl
20	23.8	95.2	25	14	US-10-058-292-11	Sequence 11, Appl
21	23.8	95.2	25	14	US-10-058-292-15	Sequence 15, Appl
22	23.8	95.2	25	14	US-10-058-292-16	Sequence 16, Appl
23	23.8	95.2	25	14	US-10-058-291-11	Sequence 11, Appl
24	23.8	95.2	25	14	US-10-058-291-15	Sequence 15, Appl
25	23.8	95.2	25	14	US-10-058-291-16	Sequence 16, Appl
26	23.8	95.2	25	14	US-10-162-879-11	Sequence 11, Appl
27	23.8	95.2	25	14	US-10-162-879-15	Sequence 15, Appl
28	23.8	95.2	25	14	US-10-162-879-16	Sequence 16, Appl
29	23.8	95.2	25	15	US-10-161-403-51	Sequence 51, Appl
30	23.8	95.2	25	15	US-10-161-403-55	Sequence 55, Appl
31	23.8	95.2	25	15	US-10-161-403-56	Sequence 56, Appl
32	23.8	95.2	25	15	US-10-300-892-15	Sequence 15, Appl
33	23.8	95.2	25	15	US-10-300-892-16	Sequence 16, Appl
34	23.8	95.2	25	15	US-10-300-892-43	Sequence 43, Appl
35	23.8	95.2	25	16	US-10-680-316-15	Sequence 15, Appl
36	23.8	95.2	25	16	US-10-680-316-16	Sequence 16, Appl
37	23.8	95.2	25	16	US-10-680-316-43	Sequence 43, Appl
38	23.8	95.2	25	17	US-10-815-730-15	Sequence 15, Appl
39	23.8	95.2	25	17	US-10-815-730-16	Sequence 16, Appl
40	23.8	95.2	25	17	US-10-815-730-43	Sequence 43, Appl
41	23.8	95.2	25	17	US-10-820-133-15	Sequence 15, Appl
42	23.8	95.2	25	17	US-10-820-133-16	Sequence 16, Appl
43	23.8	95.2	25	17	US-10-820-133-43	Sequence 43, Appl
44	23.8	95.2	25	18	US-10-161-408-42	Sequence 42, Appl
45	23.8	95.2	25	18	US-10-161-408-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1
US-09-855-797A-15
; Sequence 15, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855.797A
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-15
Query Match 95.2%; Score 23.8; DB 9; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.1;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCAGCTTTTTCACWAAGTTGG 25
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Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 2

US-09-855-797A-16
; Sequence 16, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-16

Query Match 95.2%; Score 23.8; DB 9; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.1;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAAGTTGG 25

Db 1 GTTCAGCTTTTCTGTACAAAGTTGG 25

RESULT 3

US-09-855-797A-43
; Sequence 43, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850008
; CURRENT APPLICATION NUMBER: US/09/855,797A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/296,281
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-855-797A-43

Query Match 95.2%; Score 23.8; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTTCAGCTTTTTRTACWAAGTTGG 25

RESULT 4

US-09-822-634-8
; Sequence 8, Application US/09822634
; Patent No. US20020150556A1
; GENERAL INFORMATION:
; APPLICANT: Vile, Richard G.
; APPLICANT: Harrington, Kevin
; APPLICANT: Bateman, Andrew
; APPLICANT: Murphy, Steven
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TISSUE
; FILE REFERENCE: 07039-289001
; CURRENT APPLICATION NUMBER: US/09/822,634
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/193,977
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated vector sequence
US-09-822-634-8

Query Match 95.2%; Score 23.8; DB 9; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.1;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTTCAGCTTTTCTGTACAAAGTTGG 25

RESULT 5

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; Sequence 15, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-15

Query Match 95.2%; Score 23.8; DB 9; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.1;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAAGTTGG 25

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RESULT 6
US-09-907-900-16
; Sequence 16, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-16

Query Match 95.2%; Score 23.8; DB 9; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.1;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
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Db 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||

RESULT 7
US-09-907-900-43
; Sequence 43, Application US/09907900
; Patent No. US20020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-900-43

Query Match 95.2%; Score 23.8; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
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Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 8
US-09-907-719-15
; Sequence 15, Application US/09907719
; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-719-15

Query Match 95.2%; Score 23.8; DB 9; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.1;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||

Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 9
US-09-907-719-16
; Sequence 16, Application US/09907719
; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-719-16

Query Match 95.2%; Score 23.8; DB 9; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.1;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTGTACAAAGTTGG 25
|||||

Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 10

US-09-907-719-43
; Sequence 43, Application US/09907719
; Publication No. US20020192819A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Fox, Donna K.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 43
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
US-09-907-719-43

Query Match 95.2%; Score 23.8; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAAGTTGG 25
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Db 1 GTTCAGCTTTTTRTACWAAGTTGG 25

RESULT 11

US-09-432-085-11
; Sequence 11, Application US/09432085
; Publication No. US20030100110A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 08/486,139
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-432-085-11

Query Match 95.2%; Score 23.8; DB 10; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.1;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAAGTTGG 25
|||||:|||||:|||||:|||||
Db 1 GTTCAGCTTTTCTGTACAAAGTTGG 25

RESULT 12

US-09-432-085-15
; Sequence 15, Application US/09432085
; Publication No. US20030100110A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 New York Ave., N. W. Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,085
; FILING DATE: (Herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,493
; FILING DATE: 20-JAN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,476
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,002
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: cdna

US-09-432-085-15

Query Match 95.2%; Score 23.8; DB 10; Length 25;

Best Local Similarity 88.0%; Pred. No. 1.1;

Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAAGTTGG 25

Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 13

US-09-432-085-16

Sequence 16, Application US/09432085

Publication No. US20030100110A1

GENERAL INFORMATION:

APPLICANT: Hartley, James L.

APPLICANT: Brasch, Michael A.

TITLE OF INVENTION: Recombinational Cloning Using Engineered

TITLE OF INVENTION: Recombination Sites

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C

STREET: 1100 New York Ave., N. W. Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/432,085

FILING DATE: (Herewith)

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/233,493

FILING DATE: 20-JAN-1999

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/005,476

FILING DATE: 12-JAN-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/663,002

FILING DATE: 07-JUN-1996

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/486,139

FILING DATE: 07-JUN-1995

CLASSIFICATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: cdna

US-09-432-085-16

Query Match 95.2%; Score 23.8; DB 10; Length 25;

Best Local Similarity 88.0%; Pred. No. 1.1;

Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAAGTTGG 25

Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 14

US-09-985-448-15

Sequence 15, Application US/09985448

Publication No. US20030157716A1

GENERAL INFORMATION:

APPLICANT: Hartley, James L.

APPLICANT: Brasch, Michael A.

APPLICANT: Temple, Gary F.

APPLICANT: Fox, Donna K.

TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having

TITLE OF INVENTION: Recombination Sites

FILE REFERENCE: 0942.2850004

CURRENT APPLICATION NUMBER: US/09/985,448

CURRENT FILING DATE: 2001-11-02

PRIOR APPLICATION NUMBER: US/09/177,387

PRIOR FILING DATE: 1998-10-23

PRIOR APPLICATION NUMBER: US 60/065,930

PRIOR FILING DATE: 1997-10-24

NUMBER OF SEQ ID NOS: 60

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 15

LENGTH: 25

TYPE: DNA

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: Description of Unknown Organism: recombination

OTHER INFORMATION: products

US-09-985-448-15

Query Match 95.2%; Score 23.8; DB 10; Length 25;

Best Local Similarity 88.0%; Pred. No. 1.1;

Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAAGTTGG 25

Db 1 GTTCAGCTTTTGTACAAAGTTGG 25

RESULT 15

US-09-985-448-16

Sequence 16, Application US/09985448

Publication No. US20030157716A1

GENERAL INFORMATION:

APPLICANT: Hartley, James L.

APPLICANT: Brasch, Michael A.

APPLICANT: Temple, Gary F.

APPLICANT: Fox, Donna K.

TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having

TITLE OF INVENTION: Recombination Sites

FILE REFERENCE: 0942.2850004

CURRENT APPLICATION NUMBER: US/09/985,448

CURRENT FILING DATE: 2001-11-02

PRIOR APPLICATION NUMBER: US/09/177,387

PRIOR FILING DATE: 1998-10-23

PRIOR APPLICATION NUMBER: US 60/065,930

PRIOR FILING DATE: 1997-10-24

NUMBER OF SEQ ID NOS: 60

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 16

LENGTH: 25

TYPE: DNA

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: Description of Unknown Organism: recombination

OTHER INFORMATION: products

US-09-985-448-16

Query Match 95.2%; Score 23.8; DB 10; Length 25;
 Best Local Similarity 88.0%; Pred. No. 1.1;
 Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAAGTTGG 25
 |||||:||||:||||:|||||
 Db 1 GTTCAGCTTTCTGTACAAAGTTGG 25

Search completed: November 16, 2004, 11:15:01
 Job time : 314.1 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: November 16, 2004, 03:33:04 ; Search time 1532 Seconds
(without alignments)
594.643 Million cell updates/sec

Title: US-10-820-133-43
Perfect score: 25
Sequence: 1 gttcagctttttttacwaagtgg 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_ges1:*
9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	23.8	95.2	206	5	BQ156416
C 2	23.8	95.2	299	5	BY115594
C 3	23.8	95.2	306	5	BP757615
C 4	23.8	95.2	374	5	BP754432
C 5	23.8	95.2	401	5	BP754410
C 6	23.8	95.2	409	5	BP754552
C 7	23.8	95.2	422	5	BP754464
C 8	23.8	95.2	423	5	BP754551
C 9	23.8	95.2	430	5	BP754589
C 10	23.8	95.2	432	5	BP754563
C 11	23.8	95.2	443	5	BP754508
C 12	23.8	95.2	443	5	BP754571
C 13	23.8	95.2	449	5	BP754440
C 14	23.8	95.2	472	5	BQ157398
C 15	23.8	95.2	473	5	BQ156404
C 16	23.8	95.2	482	5	BP754592
C 17	23.8	95.2	483	5	BP757892
C 18	23.8	95.2	486	5	BP754503
C 19	23.8	95.2	489	5	BP754581
C 20	23.8	95.2	546	5	BP754439
C 21	23.8	95.2	567	5	BP754491
C 22	23.8	95.2	597	4	BA422679
C 23	23.8	95.2	645	5	BP754484
C 24	23.8	95.2	671	5	BP754388

C 25	23.8	95.2	672	5	BP754535
C 26	23.8	95.2	674	5	BP754519
C 27	23.8	95.2	689	5	BP754572
C 28	23.8	95.2	695	8	AQ991039
C 29	23.8	95.2	712	8	AQ990809
C 30	23.8	95.2	731	5	BP758121
C 31	23.8	95.2	743	8	AQ990346
C 32	23.8	95.2	764	8	AQ990110
C 33	23.8	95.2	769	8	AQ990470
C 34	22.8	91.2	395	8	AQ991303
C 35	22.8	91.2	664	8	AQ991011
C 36	22.8	91.2	751	8	AQ989566
C 37	21.2	84.8	672	8	AQ990864
C 38	21.2	84.8	753	8	AQ990861
C 39	21.2	84.8	770	8	AQ991774
C 40	21.2	84.8	791	8	AQ991791
C 41	21.2	84.8	808	8	AQ990388
C 42	21.2	84.8	821	9	CL672759
C 43	21.2	84.8	875	9	CL688994
C 44	20.8	83.2	87	6	CB400039
C 45	20.8	83.2	90	6	CB392047

ALIGNMENTS

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LOCUS BQ156416 206 bp mRNA linear EST 24-APR-2002
DEFINITION NF092F02IR1F1027 Irradiated Medicago truncatula cDNA clone
ACCESSION BQ156416
VERSION BQ156416.1 GI:20293475
KEYWORDS EST.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 206)
Torres-Jerez, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.,
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula irradiated library
Unpublished (2001)
JOURNAL Contact: May GD
COMMENT Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 224 6650
Fax: 580 224 6692
Email: gdmay@noble.org
Insert Length: 206 Std Error: 0.00
Plate: 092 row: F column: 02
Seq primer: TCACACGGAACACGCTATGAC.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF092F02IR"
/tissue_type="seedlings"
/dev_stage="seedling"
/clone_lib="Irradiated"
/note="Vector: Lambda Zap; Seedlings were exposed either
to 100 Gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation.
Gamma-irradiated samples were harvested at 6, 12, 24 and
48 hours after treatment. UV-irradiated samples were
harvested 24 hours post-treatment. cDNA was prepared from
polyA+ enriched, pooled samples of equivalent amounts of
total RNA from each sample. The cDNA was directionally
ligated into the Uni-Zap XR vector (Stratagene) and

packaged using the Gigapack III Gold packaging extracts. Phagmids containing cDNA inserts were in vivo excised from the recombinant Uni-ZAP XR vector using EXassist helper phage and the E. coli strain XL1-Blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."

```

ORIGIN
Query Match      95.2%; Score 23.8; DB 5; Length 206;
Best Local Similarity 88.0%; Pred. No. 13;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAAGTTGG 25
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Db 167 GTTCAGCTTTTATCTACTAAGTTGG 143

RESULT 2
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LOCUS BY115594 RIKEN full-length enriched, 18 days embryo whole body Mus
DEFINITION musculus cDNA clone L430040C03 5', mRNA sequence.
ACCESSION BY115594
VERSION BY115594.1 GI:26226695
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 299)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Oato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Mateuda, H.,
Bacalov, S., Beisel, K. W., Blake, J. A., Bratt, D., Brusci, V.,
Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,
Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Kongaya, A.,
Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W. J., Perlea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J. U., Oi, D., Ramachandran, S.,
Ravasi, T., Read, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M.,
Sandelin, A., Schneider, C., Sempile, C. A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Haru, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
Rogers, J., Birney, E. and Hayaehizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
22354683
12466851
Contact: Yoshihide Hayaehizaki
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp URL:http://genome.gsc.riken.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,

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Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
Hayaehizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
FEATURES
source
Location/Qualifiers
1..299
/organism="Mus musculus"
/mol_type="mRNA"
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Best Local Similarity 88.0%; Pred. No. 14;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db 246 GTTCAGCTTTTATCTACTAAGTTGG 270

RESULT 3
LOCUS BP757615/c BP757615 306 bp mRNA linear EST 08-JUL-2004
DEFINITION BP757615 mouse (C57BL/6) pancreatic islet library with
recombination-based method Mus musculus cDNA clone mib04031 3',
mRNA sequence.
ACCESSION BP757615
VERSION BP757615.1 GI:50077505
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 306)
Nishimura, M., Yokoi, N., Miki, T., Horikawa, Y., Yoshioka, H.,
Takeda, J., Ohara, O. and Seino, S.
Construction of a multi-functional cDNA library specific for mouse
pancreatic islets and its application to microarray
Unpublished (2004)
Contact: Susumu Seino
Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.
Location/Qualifiers
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/clone_lib="mouse (C57BL/6) pancreatic islet library with
recombination-based method"

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Best Local Similarity 88.0%; Pred. No. 14;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db 109 GTTCAGCTTTTGTACAAAGTTGG 85

RESULT 4
BP754432/c
LOCUS BP754432 374 bp mRNA linear EST 08-JUL-2004
DEFINITION BP754432 mouse (C57BL/6) pancreatic islet library with
recombination-based method Mus musculus cDNA clone mial0061 3',
mRNA sequence.
ACCESSION BP754432
VERSION BP754432.1 GI:50074322
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 374)
Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
Takeda,J., Ohara,O. and Seino,S.
Construction of a multi-functional cDNA library specific for mouse
pancreatic islets and its application to microarray
Unpublished (2004)
JOURNAL
COMMENT Contact: Susumu Seino
Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.
Location/Qualifiers
1..374
/organism="Mus musculus"
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/clone="mial0061"
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/clone_lib="mouse (C57BL/6) pancreatic islet library with
recombination-based method"

ORIGIN
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Best Local Similarity 88.0%; Pred. No. 15;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db 73 GTTCAGCTTTTGTACAAAGTTGG 49

RESULT 5
BP754410/c
LOCUS BP754410 401 bp mRNA linear EST 08-JUL-2004
DEFINITION BP754410 mouse (C57BL/6) pancreatic islet library with
recombination-based method Mus musculus cDNA clone mial0045 3',
mRNA sequence.
ACCESSION BP754410
VERSION BP754410.1 GI:50074300
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 401)
Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
Takeda,J., Ohara,O. and Seino,S.
Construction of a multi-functional cDNA library specific for mouse
pancreatic islets and its application to microarray
Unpublished (2004)
JOURNAL
COMMENT Contact: Susumu Seino
Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.
Location/Qualifiers
1..401
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/mol_type="mRNA"
/strain="C57BL/6"
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/clone="mial0045"
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recombination-based method"

ORIGIN
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Best Local Similarity 88.0%; Pred. No. 15;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAAGTTGG 25
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Db 73 GTTCAGCTTTTGTACAAAGTTGG 49

RESULT 6
BP754552/c
LOCUS BP754552 409 bp mRNA linear EST 08-JUL-2004
DEFINITION BP754552 mouse (C57BL/6) pancreatic islet library with
recombination-based method Mus musculus cDNA clone mial1051 3',
mRNA sequence.
ACCESSION BP754552
VERSION BP754552.1 GI:50074442
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 409)
Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
Takeda,J., Ohara,O. and Seino,S.
Construction of a multi-functional cDNA library specific for mouse
pancreatic islets and its application to microarray
Unpublished (2004)
JOURNAL
COMMENT Contact: Susumu Seino
Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.
Location/Qualifiers
1..409
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source

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 /dev stage="adult"
 /clone.lib="mouse (C57BL/6) pancreatic islet library with
 recombination-based method"

ORIGIN

Query Match 95.2%; Score 23.8; DB 5; Length 443;
 Best Local Similarity 88.0%; Pred. No. 15;
 Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAAGTTGG 25
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Db 89 GTTCAGCTTTTGTACAAAGTTGG 65

RESULT 13
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LOCUS
 DEFINITION BP754440 mouse (C57BL/6) pancreatic islet library with
 recombination-based method Mus musculus cDNA clone mial0069 3',
 mRNA sequence.

ACCESSION BP754440 449 bp mRNA linear EST 08-JUL-2004

VERSION BP754440.1 GI:50074330

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 449)
 Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
 Takeda,J., Ohara,O. and Seino,S.

TITLE Construction of a multi-functional cDNA library specific for mouse
 pancreatic islets and its application to microarray

JOURNAL Unpublished (2004)

COMMENT Contact: Susumo Seino
 Division of Cellular and Molecular Medicine
 Kobe University Graduate School of Medicine
 7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
 Tel: 81-78-382-5360
 Fax: 81-78-382-5370
 Email: seino@med.kobe-u.ac.jp.

FEATURES
 Location/Qualifiers
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ORIGIN

Query Match 95.2%; Score 23.8; DB 5; Length 449;
 Best Local Similarity 88.0%; Pred. No. 15;
 Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db 73 GTTCAGCTTTTGTACAAAGTTGG 49

RESULT 14
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LOCUS
 DEFINITION BQ157398 472 bp mRNA linear EST 24-APR-2002
 NF104D071R1F1062 Irradiated Medicago truncatula cDNA clone
 NF104D071R 5', mRNA sequence.

ACCESSION BQ157398

VERSION BQ157398.1 GI:20294457

KEYWORDS EST.

SOURCE Medicago truncatula (barrel medic)

ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosoid 1; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.

REFERENCE 1 (bases 1 to 472)
 Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
 Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.

TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 Medicago truncatula irradiated library

JOURNAL Unpublished (2001)

COMMENT Contact: May GD
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 224 6650
 Fax: 580 224 6692
 Email: gdmay@noble.org

Insert Length: 472 Std Error: 0.00
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Seq primer: TCACACAGGAACAGCTATGAC.

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 to 100 Gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation.
 Gamma-irradiated samples were harvested at 6, 12, 24 and
 48 hours after treatment. UV-irradiated samples were
 harvested 24 hours post-treatment. cDNA was prepared from
 polyA+ enriched, pooled samples of equivalent amounts of
 total RNA from each sample. The cDNA was directionally
 ligated into the Uni-Zap XR vector (Stratagene) and
 packaged using the GigaPack III Gold packaging extracts.
 Phagemids containing cDNA inserts were in vivo excised
 from the recombinant Uni-Zap XR vector using ExAseist
 helper phage and the E. coli strain XLI-Blue MRF'
 (Stratagene). Excised plasmids were plated using SOLR
 cells."

ORIGIN

Query Match 95.2%; Score 23.8; DB 5; Length 472;
 Best Local Similarity 88.0%; Pred. No. 15;
 Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db 380 GTTCAGCTTTTATACTAAGTTGG 356

RESULT 15
 BQ156404/c

LOCUS
 DEFINITION BQ156404 473 bp mRNA linear EST 24-APR-2002
 NF0925031R1F1023 Irradiated Medicago truncatula cDNA clone
 NF0925031R 5', mRNA sequence.

ACCESSION BQ156404

VERSION BQ156404.1 GI:20293463

KEYWORDS EST.

SOURCE Medicago truncatula (barrel medic)

ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

1 (bases 1 to 473)

Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation

Medicago truncatula irradiated library

Unpublished (2001)

Contact: May GD

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Tel: 580 224 6650

Fax: 580 224 6692

Email: gdmay@noble.org

Insert Length: 473 Std Error: 0.00

Plate: 092 row: E column: 03

Seq primer: TCACACAGGAAACAGCTATGAC.

FEATURES

source

Location/Qualifiers

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/note="Vector: Lambda Zap; Seedlings were exposed either to 100 Gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation. Gamma-irradiated samples were harvested at 6, 12, 24 and 48 hours after treatment. UV-irradiated samples were harvested 24 hours post-treatment. cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from each sample. The cDNA was directionally ligated into the Uni-zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-ZAP XR vector using ExAssist helper phage and the E. coli strain XL1-Blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."

ORIGIN

Query Match 95.2%; Score 23.8; DB 5; Length 473;

Best Local Similarity 88.0%; Pred. No. 15;

Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCAGCTTTTTRTACWAGTTGG 25

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Db 381 GTTCAGCTTTTATACTAGTTGG 357

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